CCAGGTCCAACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA ${\tt CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC}$ AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCGGCCACCATGGCCACGCCTGGGC TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGGGAGGCACAGGTGGCCCCCACCACCCGGAGG $\mathtt{AGCAGCTCCTGCCCCTGTCCGGGGGG}$ AGGCCACCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT TCTGGTGTTGGCAGTGGGCGCACAGAGCACGCCTACCGGCCCGGCCGTTAGGGTGTGTGCT GTCCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCGTGCAGCGTGTGTACCAGCCCTTCC TCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATTTATAGGACCGCCTAC CGCCGCAGCCTGGGCTGGCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAG ## GACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAG GGAGCTGTGTCCAGCCTGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG # TCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGC $\tt CGGCAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG$ O'l TGCCCAAGGGAGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAG GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAAGCTGCAGCTGGTGCT GGCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC CTGGAGGAGCAGCTGGGGTCCTGCTCCAGAGAAAGACTCGTGACTGCCCAGCGCCCCAGG CTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATGCCCCTGCCCAACATGCTGGGGGTC CCACCCTGGCTACCCCCACCCTGGTTACCCCAACGCCATCCCAAGGCCAGGTGGGCCCTCA GCTGAGGGAAGGTACGAGTTCCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCC CGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAA AGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGT TACAAAT

40

40

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGDPV SESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC GAAICQPPCRNGGSCVQPGRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCW EGHSLSADGTLCVPKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLAS QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation sites. amino acids 93-97, 270-274

N-myristoylation sites.

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163, 1 191-197, 265-271

Amidation site.

amino acids 26-30

Aspartic acid and asparagine hydroxylation site.

amino acids 152-164

Cell attachment sequence.

amino acids 130-133

EGF-like domain cysteine pattern signature.

amino acids 123-135

GTCAGCCCACGGCGGGGACT**ATG**GTGAAATTCCCGGCGCTCACGCACTACTGGCCCCTGATC CGGTTCTTGGTGCCCCTGGGCATCACCAACATAGCCATCGACTTCGGGGAGCAGGCCTTGAA CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT ACTCCCTCATGAAGTTCTTCACGGGTCCCATGAGTGACTTCAAAAATGTGGGCCTGGTGTTT GTGAACAGCAAGAGACAGGACCAAAGCCGTCCTGTGTATGGTGGTGGCAGGGGCCATCGC TGCCGTCTTTCACACACTGATAGCTTATAGTGATTTAGGATACTACATTATCAATAAACTGC ${\tt ACCATGTGGACGAGTCGGTGGGGAGCAAGACGAGAAGGGCCTTCCTGTACCTCGCCGCCTTT}$ CCTTTCATGGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAAACACAAATACAGTTT CCTGGTGGGATGTGCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTTGTAGCCATTTTGC TTCACAGTCACCTGGAATGCCGGGAGCCCCTGCTCATCCCGATCCTCCTTGTACATGGGC GCACTTGTGCGCTGCACCACCCTGTGCCTGGGCTACTACAAGAACATTCACGACATCATCCC GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA CCCTGTGGGTCACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTCG ACAAGAATAACCCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCAGCCCACATC AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTTGGAC ACCCAACGTGTCTGAGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC TCTGTGTTGTTCCTTTGCGGATCTTCTCCTTCTTCCCAGTTCCAGTCACAGTGAGGGCGCAT CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTCCTTGCCCCCAGCTCTGTGCTGCG GATCATCGTCCTCATCGCCAGCCTCGTGGTCCTACCCTACCTGGGGGTGCACGGTGCGACCC TGGGCGTGGGCTCCCTGGCGGGCTTTGTGGGAGAATCCACCATGGTCGCCATCGCTGCG ## GAAAGAGGCCTTGATTTAAAGGTTTCGTGTCAATTCTCTAGCATACTGGGTATGCTCACACT TTCATACCCCTGCCTCACGAAAACCCAAAAGACACAGCTGCCTCACGGTTGACGTTGTCCC ## TCCTCCCTGGACAATCTCCTCTTGGAACCAAAGGACTGCAGCTGTGCCATCGCGCCTCGGT CACCCTGCACAGCAGGCCACAGACTCTCCTGTCCCCCTTCATCGCTCTTAAGAATCAACAGG TTAAAACTCGGCTTCCTTTGATTTGCTTCCCAGTCACATGGCCGTACAAAGAGATGGAGCCC CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACACATGCAG GAGGCGGGTGGCACGCTGCAGCCCGGAGTCCCCGTTCACACTGAGGAACGGAGACCTGTGAC CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTTGAAATGCCCCGGG GGCAGCAAACTGACATGGTTGAATGATAGCATTTCACTCTGCGTTCTCCTAGATCTGAGCAA GCTGTCAGTTCTCACCCCCACCGTGTATATACATGAGCTAACTTTTTTAAATTGTCACAAAA CTTTCCTGAAGGTCGCATTAGAGCGAGTCACATGGAGCATCCTAACTTTGCATTTTAGTTTT TACAGTGAACTGAAGCTTTAAGTCTCATCCAGCATTCTAATGCCAGGTTGCTGTAGGGTAAC TTTTGAAGTAGATATTACCTGGTTCTGCTATCCTTAGTCATAACTCTGCGGTACAGGTAA TTGAGAATGTACTACGGTACTTCCCTCCCACACCATACGATAAAGCAAGACATTTTATAACG ATACCAGAGTCACTATGTGGTCCTCCCTGAAATAACGCATTCGAAATCCATGCAGTGCAGTA TATTTTTCTAAGTTTTGGAAAGCAGGTTTTTTCCTTTAAAAAAATTATAGACACGGTTCACT AAATTGATTTAGTCAGAATTCCTAGACTGAAAGAACCTAAACAAAAAAATATTTTAAAGATA TAAATATATGCTGTATATGTTATGTAATTTATTTTAGGCTATAATACATTTCCTATTTTCGC ATTTTCAATAAAATGTCTCTAATACAAAAA

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF
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GSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC
REPLLIPILSLYMGALVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL
ATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN
KLVSTSNTVTAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLR
IFSFFPVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYLGVHGATLGVGSLL
AGFVGESTMVAIAACYVYRKQKKKMENESATEGEDSAMTDMPPTEEVTDIVEMREENE

Transmembrane domains:

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374, 408-423, 431-445

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTGTGGGTCACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTTATCCTGCTTTCG
ACAAGAATAACCCCAGCAACAAACTGGTGAGCACGAGCAACACAGTCACGGCGGCCCACATC
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC
ACCCAACGTGTCTGNGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTTGCAGAAC
TCTGTGTTGTTCCTTTGCGGATCTTCTCCTTCTTCCCAGTTCCAGTCACAGTGAGGGCGCAT
CTCACCGGGTGGCTGATGACACACTGAAGAAAACCTTCGTC

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG
GAGCAGGGCAAAACAGTNACGGGCAGCCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAATTTTGAT
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTCCTTTGCGGATTTTCT
CCTTTTTCCCAGTTCCAGTCACAGNGAGGGCGCATCTCACCGGGNGGNTGATGACANTGAAG
AAAACCTTTGTCCTTGCCCCCAGCTNTTTGGTGCGGATCATTGTCCTNATNGCCAGCCTTGT
GGTCCTACCCTGGGGGTGCACGGTGCGACCCTGGGCGTGGGTTCCCTCCTGGCGGCCA

TATTCCCAGTTCCGGTCACGGGGAGGGCGCATNTCACCGGGTGGCTGANGACACTGAAGAAA ACCTTNGTCCTTGCCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT CCTACCCTACCTGGGGGTGCACGGTGAGAC

GCCCGCGCCCGGCCCGGGCCCCGAAGCCGGGAGCCACCGCC<u>ATG</u>GGGGCCTGCCTGGGA GCCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG $\tt CTGCTGCCCGCCAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCCTCTTCC$ TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTG CCCTGGGTGTGTGAGGAGGGGCCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGG $\tt CTCCCTGCTTGGCTACCGCGTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCT$ TCTTTTCACCCTGCTCATGCTCTGCGTGAGCAGCCGGGACCCCCGGGCTGCCATCCAG AATGGGTTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACAT TCCTCATCCAGCTGGTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGC AAGGCCGAGGAGTGCGATTCCCGTGCCTGGTACGCAGGCCTCTTCTTCTTCACTCTCTT CTACTTGCTGTCGATCGCGGCCGTGGCGCTGATGTTCATGTACTACACTGAGCCCAGCGGCT GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT GCTGTCCTGCCCAAGGTCCAGGACGCCCAACTCGGGTCTGCTGCAGGCCTCGGTCAT CACCCTCTACACCATGTTTGTCACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA ACCCCCATTTGCCAACCCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG ACCCAGTGGTGGGATGCCCCGAGCATTGTGGGCCTCATCATCTTCCTCCTGTGCACCCTCTT CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCC $\mathtt{TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCT$ GGCCTCACTGCACGTCATGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA TGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC TACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGC**TGA**GGCAGCCT CACAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCT GCCCCTCCCCACACCAATCAGCCAGGCTGAGCCCCCACCCCTGCCCCAGCTCCAGGACCTG CCCCTGAGCCGGGCCTTCTAGTCGTAGTGCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA TGCCCATACTCAGCATCTCGGATGAAAGGGCTCCCTTGTCCTCAGGCTCCACGGGAGCGGG ${\tt CTGCTGGAGAGCGGGGAACTCCCACCACAGTGGGGCATCCGGCACTGAAGCCCTGGTGTT}$ ${\tt CCTGGTCACGTCCCCAGGGGACCCTGCCCCCTTCCTGGACTTCGTGCCTTACTGAGTCTCT}$ AAGACTTTTTCTAATAAACAAGCCAGTGCGTGTAAAAAAA

MGACLGACSLLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVE
SQLYKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFTLLMLCVSSSRD
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHSW
NQRWLGKAEECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFC
VCVSIAAVLPKVQDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVA
ACEGRAFDNEQDGVTYSYSFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVWVKICAS
WAGLLLYLWTLVAPLLLRNRDFS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257, 272-283, 324-340, 391-406, 428-444

GAGCGAGGCCGGGGACTGAAGGTGTGGGTGTCGAGCCCTCTGGCAGAGGGTTAACCTGGGTC AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGA AGTCCTGAGCGCTCAAGTTTGTCCGTAGGTCGAGAGAGGCCATGGAGGTGCCGCCACCGGC ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCCCCGAGTCTTTGCTGCCGAAGCTG ${\sf TGACTGCCGATTCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCC}$ TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGCATCATTGGCTGGG TGTATGGGGGAATACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT CATTCGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTTTGTGACTATATTCAACACAG TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAATTGCAGGA ${ t AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTG}$ GTGAGACTGTTCAGGAAAGAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACTGGAA GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAACC CTTCAGTAATAGATAAACAAGACAAGGAC**TGA**AAGTGCTCTGAAACTCACTGGAGA TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTTTTCTTTTCTT GCAGTAAATAAAACATTTCGCAAAAGATTAAAGTTGAATTTTACAGTTT

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><subunit 1 of 1, 285 aa, 1 stop

><MW: 32190, pI: 9.03, NX(S/T): 2

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Important Features:

Signal Peptide:

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT
AACCGGTTTGATGCTGCACATCTGCACATCGTGCTGCCACACGAGGCTTCATTCGTTCATG
GCTGGCGCCGAACC

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT
TTTTCTGTAGAGCATTGTGCCTATTTCCCCGAGTTTTTGCTGCCGAAGCTGTGACTGCCGAT
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGATTTCAAAGG
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA
ATACCAGCTTTTATTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA
TAACC

GCGTTGCTGCCCCGCCTGGGCCAGGCCCCAAAGGCAAGGACAAAGCAGCTGTCAGGGAACCT CCGCCGGAGTCGAATTTACGTGCAGCTGCCGGCAACCACAGGTTCCAAGATGGTTTGCGGGG GCTTCGCGTGTTCCAAGAACTGCCTGTGCGCCCTCAACCTGCTTTACACCTTGGTTAGTCTG $\tt CTGCTAATTGGAATTGCTGCGTGGGGCATTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGT$ CGGCGTGGTCATTGCAGTGGGCATCTTCTTGTTCCTGATTGCTTTAGTGGGTCTGATTGGAG GTTCAGTTTTCTGTATCTTGCGCTTGTTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCT GGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCT GTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTCTGGCTAGCTGTGTTAAAAGTGACCAC TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGAGATTTGTTGG TGGCATTGGCCTGTTCTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACCTACAGATACA GGAACCAGAAAGACCCCCGCGCGAATCCTAGTGCATTCCTT**TGA**TGAGAAAACAAGGAAGAT TTCCTTTCGTATTATGATCTTGTTCACTTTCTGTAATTTTCTGTTAAGCTCCATTTGCCAGT TTAAGGAAGGAAACACTATCTGGAAAAGTACCTTATTGATAGTGGAATTATATATTTTTACT CTATGTTTCTCTACATGTTTTTTTTTTCTTTCCGTTGCTGAAAAATATTTGAAACTTGTGGTCTC TGAAGCTCGGTGGCACCTGGAATTTACTGTATTCATTGTCGGGCACTGTCCACTGTGGCCTT TCTTAGCATTTTTACCTGCAGAAAAACTTTGTATGGTACCACTGTGTTGGTTATATGGTGAA TCTGAACGTACATCTCACTGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCCTAC TGGAAAAAGAGTGGAAATTTATTAAAATCAGAAAGTATGAGATCCTGTTATGTTAAGGGAAA TCCAAATTCCCAATTTTTTTTGGTCTTTTTAGGAAAGATTGTTGTGGTAAAAAGTGTTAGTA TAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAAATAGTTAT GTCTTAGGAAATTGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTGGTTT CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCATCAGAATGGAACGAGTTT TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTTATAATAATTTGAAGTCTAA AAGACTGCATTTTTAAACAAGTTAGTATTAATGCGTTGGCCCACGTAGCAAAAAGATATTTG ATTATCTTAAAAATTGTTAAATACCGTTTTCATGAAATTTCTCAGTATTGTAACAGCAACTT GTCAAACCTAAGCATATTTGAATATGATCTCCCATAATTTGAAATTGAAATCGTATTGTGTG ATTAAAAGAAAGTAATGGAAG

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><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

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Signal Peptide:

amino acids 1-34

Transmembrane domains:

amino acids 47-63, 72-95 and 162-182

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTATATGATTATTCTGTAANT
TGTATTTATTGTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT
NTAAACTGCTGTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTNTGGCTAGCTGTGTTAA
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA
GATTTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC
TACAGATACAGGAACCAG

AATCCCAAATTCCCCAATTTTTTTGGNCTTTTTAGGGAAAGATGTGTTGTGGTAAAAAGTGT
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG
TTATGTCTTAGGAAATTGTGGTTTAATTTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG
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AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG
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CCACTTGC

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TGACTCCGCAAATGACATCCCAGAGAAATCCTAAACTGCTGTGGGTTCCGAAGTGTTAACCC
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA
TCATAGGAGAATATGC

CAGTCACCATGAAGCTGGGCTGTGTCCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG CTCTGGGTGGCCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGT CTGCACTGAGGAGGAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT TCCAGGTCAAGGCCTACACTTTCAGTGAACCCTTCCACCTGATTGTGTCCTATGACTGGCTG ATCCTCCAAGGTCCAGCCAAGCCAGTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC CCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC TGCAGTGGCATCTTCCAGAGCCCTGGTCCTGGGATCCCAGAAACAGCATCTGTTGTGGCTAT CACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG CAGGAAGCCCCATGACCCTGAGTTGTCAGACAAAGTTGCCCCTGCAGAGGTCAGCTGCCCGC CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCATACTGGTGTGAGGCAGCCACTGAGG ACAACCAAGTTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT GCTGCACCTCCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAACTGCTCCTGA GGAGGCCCCTGGGCCTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATG CAGGATGTGAGAGTCCTCCTCGGTCACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA GAAGCCTGGGACCACAAAGGCTACTGCTGAA**TAG**AAGTAAACAGTTCATCCATGATCTCACT TAACCACCCCAATAAATCTGATTCTTTATTTTCTCTTCCTGTCCTGCACATATGCATAAGTA CTTTTACAAGTTGTCCCAGTGTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAAATAAATTT ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAA CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGCCCCCCAGAGGACA TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGGGTTGGGGGATGGTGGGATGT GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAG GGCAGTACCCCACAACGAAAAATAATCTGGCCCAAAATGTCAGTTGTACTGAGTTTGAGAAA CCCCAGCCTAATGAAACCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT TATCTCTTTCCAGCCTCATTCAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGCTATG GTCTGTTCTTTAGTTCTAGTTTGTATCCCCTCAAAAGCCATTATGTTGAAATCCTAATCCCC AAGGTGATGGCATTAAGAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCCTTCCACCAT ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAAACAGCTGTCGCCAAACACCG ACTCTGTCGTTGCCTTGATCTTGAACTTCCAGCCTCCAGAACTATGAGAAATAAAATTCTGG TTGTTTGTAGCCTAA

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><subunit 1 of 1, 359 aa, 1 stop

><MW: 38899, pI: 5.21, NX(S/T): 0

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KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRCQAWQDWPLTQVTFYRDGSALGPPGP
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS
PMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ
VWKQSPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPEEAPGPLPPPPTPSSEDPGFSSPL
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

CCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGGGCCACCAGAAGTT TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAGGACAGAAGTAGCTCTGGCTGTG**ATG**GGG ATCTTACTGGGCCTGCTACTCCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT GGAAGTGCCAGAGAGTGTAACAGGACCTTGGAAAGGGGATGTGAATCTTCCCTGCACCTATG ACCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCT GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACCAGGGCCG CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCCTGGAGATGG ATGACCGGAGCCACTACACGTGTGAAGTCACCTGGCAGACTCCTGATGGCAACCAAGTCGTG AGAGATAAGATTACTGAGCTCCGTGTCCAGAAACTCTCTGTCTCCAAGCCCACAGTGACAAC TGGCAGCGGTTATGGCTTCACGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC GGGGTTCTCCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACCAGGAACCCATC AAAGTAGCAACCCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC TGGAGAGACCAGTGCTGGGCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCT CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTCGGAAGACATCCCAA CAAGAGCATGTCTACGAAGCAGCCAGG**TAA**GAAAGTCTCTCCTCTTCCATTTTTGACCCCGT CCCTGCCCTCAATTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGGTGTGGCACAGACCC AATCCTAAGGCCGGAGGCCTTCAGGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT CCAGTGATGAGCCAACTTCCCAGAATCTGGGCAACAACTACTCTGATGAGCCCTGCATAGGA TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTTAAAAATGCCCCATTAGGC CAGGATCTGCTGACATAATTGCCTAGTCAGTCCTTGCCTTCTGCATGGCCTTCTTCCCTGCT ACCTCTCTTCCTGGATAGCCCAAAGTGTCCGCCTACCAACACTGGAGCCGCTGGGAGTCACT GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTTGGCTCTGG GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTAAATACCAGAGGGAAGATG CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT TTCTCTTTCTTCAGGGCCAGACAGCTTTTAATTGAAATTGTTATTTCACAGGCCAGGGTTCA **ATCATAACAGC**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416</pre>

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

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VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQQTNNQE
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTTMT
YPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFTMAYIMLCRKT
SQQEHVYEAAR

Signal Sequence:

amino acids 1-19

Glycosaminoglycan attachment site:

amino acids 149-152

Transmembrane domain:

amino acids 282-300

GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCCCAGCTCGCCCGAGGTCCGTCGGA GGCGCCGGCCCCGGAGCCAAGCAGCAACTGAGCGGGAAGCGCCCGCGTCCGGGGATC GGG<u>ATG</u>TCCCTCCTCCTCTCTCTCTAGTTTCCTACTATGTTGGAACCTTGGGGACTCA CACTGAGATCAAGAGGGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA GTGGTGATCACTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG AGTGGCCTTTGCTTCCAATTTCCTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGC CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTGTGTATT ACTGGCAGCGAATCCGAGAGAAAGAGGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT GACTACAACCACCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA CCAGTGCACAGCAGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACTGTACAGT ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT CCTCTTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCCTCCACTCGCTCCACAGCAAAT ACGGTCTGAATTACAATGGACTTGACTCCCACGCTTTCCTAGGAGTCAGGGTCTTTGGACTC TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA GTGAGCATTGCACGGAACAGATTCAGATGAGCATTTTCCTTATACAATACCAAACAAGCAAA AGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG AGGTGAATATACCTAAAACTTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTCACAATT TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTTCTATGCATTTCTGCAAACTTATTGGATT ATTAGTTATTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC TGAGCTAACCACTTCTAAGAAACTCCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC TTCATTTGTCATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAAC TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCATGATGTT ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCCCTCAAAT CAGATGCCTCTAAGGACTTTCCTGCTAGATATTTCTGGAAGGAGAAAATACAACATGTCATT TATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA CCCAACATACCATTATAGTCTCTTCTTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

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><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

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Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

GTCGTTCCTTTGCTCTCCGCGCCCAGTCCTCCTCCTGGTTCTCCTCAGCCGCTGTCGGAGGAGAGCACCCGGA GACGCGGCTGCAGTCGCGGCGGCTTCTCCCCGCCTGGGCGGCCTCGCCGCTGGGCAGGTGCTGAGCGCCCCTAG GCCCGGGAGGCGGCGGTGGATGCGGCGCTGGGCAGAAGCAGCCGCCGATTCCAGCTGCCCCGCGCGCCCCGGGCG $\tt CCCCTGCGAGTCCCCGGTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCCTGCAGCCGCATC$ GCCCGCCGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCCTGCTTGGATTCCTTAGCACCACACCACAGCTCAG CCAGAACAGAAGGCCTCGAATCTCATTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCT GTGGGGACCTTTACCAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAATG ATTGAGAAATTACCTTGTGCTGCCTTGACTGACCGAGAATGCACTTGCCCACCTGGCATGTTCCAGTCTAACGCT ACCTGTGCCCCCATACGGTGTGTCCTGTGGGTTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG TGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCTTCTAGTGTGATGAAATGCAAAGCATACACAGACTGT $\tt CTGAGTCAGAACCTGGTGGTGATCAAGCCGGGGACCAAGGAGACAACGTCTGTGGCACACTCCCGTCCTTC$ TCCAGCTCCACCTCACCTTCCCCTGGCACAGCCATCTTTCCACGCCCTGAGCACATGGAAACCCATGAAGTCCCT TCCTCCACTTATGTTCCCAAAGGCATGAACTCAACAGAATCCAACTCTTCTGCCTCTGTTAGACCAAAGGTACTG CCAAACCTTCAGGTAGTCAACCACCAGCAAGGCCCCCACCACAGACACATCCTGAAGCTGCTGCCGTCCATGGAG GCCACTGGGGGCGAGAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAG TGCAGTATCCGGAAAAGCTCGAGGACTCTGAAAAAGGGGCCCCGGCAGGATCCCAGTGCCATTGTGGAAAAGGCA GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT ATCCGGGGCCCGAGCCAGCCTCGCCCAGCTAATTAGCGCCCTGCGCCAGCACCGGAGAAACGATGTTGTGGAG AAGATTCGTGGGCTGATGGAAGACACCACCCAGCTGGAAACTGACAAACTAGCTCTCCCGATGAGCCCCAGCCCG ${\tt CAGGACAAGAACAAGGGCTTCTTCGTGGATGAGTCGGAGCCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCC}$ ATTCCCCAGGCTGAGGACAAACTAGACCGGCTATTCGAAATTATTGGAGTCAAGAGCCAGGAAGCCAGACC $\tt CTCCTGGACTCTGTTTATAGCCATCTTCCTGACCTGCTG{\color{blue}{TAG}}{\color{blue}{TAG}}{\color{blue}{AACATAGGGATACTGCATTCTGGAAATTACTCA}$ TCTCTCTCTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTATAAGCCTTTGCCAGGTGTAACTGTTGTGAA ATACCCACCACTAAAGTTTTTTTAAGTTCCATATTTTCTCCATTTTTGCCTTCTTATGTATTTTCAAGATTATTCTG TGCACTTTAAATTTACTTAACTTACCATAAATGCAGTGTGACTTTTCCCACACACTGGATTGTGAGGCTCTTAAC TTCTTAAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTCACACCTACTTTTT AAAAACAAATATTATTACTATTTTTTATTATTGTTTGTCCTTTATAAATTTTCTTAAAGATTAAGAAAATTTAAGA CCCCATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTTCATATTCATGG CTGAAACTTGACCACACTATTGCTGATTGTATGGTTTTCACCTGGACACCGTGTAGAATGCTTGATTACTTGTAC TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT GACAACTGGGCCACCAAAGAACTTGAACTTCACCTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACTTT GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCCAGCTTTGCTTTAAAAGATGTCTTG TTTTTTATATACACATAATCAATAGGTCCAATCTGCTCTCAAGGCCTTGGTCCTGGTGGGATTCCTTCACCAATT ACTTTAATTAAAAATGGCTGCAACTGTAAGAACCCTTGTCTGATATATTTTGCAACTATGCTCCCATTTACAAATG AAAAAAAA

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><subunit 1 of 1, 655 aa, 1 stop

><MW: 71845, pI: 8.22, NX(S/T): 8

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ALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRKKGTETEDVRCKQCARGTFSDVPSSVMKC
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHIL
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIVVCSIRK
SSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNREKWIYYCNGHGIDILKLVAAQVGSQWKDIY
QFLCNASEREVAAFSNGYTADHERAYAALQHWTIRGPEASLAQLISALRQHRRNDVVEKIRG
LMEDTTQLETDKLALPMSPSPLSPSPIPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLL
RCDSTSSGSSALSRNGSFITKEKKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ
AEDKLDRLFEIIGVKSQEASQTLLDSVYSHLPDLL

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTGGGA CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCAC $\mathtt{CATG}\mathtt{GGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTTGGCC$ TTGATGATTTGAAAATAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG TCACTGCTGCCATTGAAGTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC GAGTACCGCTGTGTCCGGGTGGTCGGTCAGAATGCCGTGCTCCAGGTGTTCACAGCTGCTTC GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCCAAC TGGGTTTCCCAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGCAGTTC CGGGAGGAGTTTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCAGTGCACAGCCT TGGCCCTGGCAGGCCAGCCTTCAGTTCCAGGGCTACCACCTGTGCGGGGGCTCTGTCATCAC GCCCCTGTGGATCATCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGA CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAG ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCCCTGCCCAACTCTGAAGAGA ACTTCCCCGATGGAAAAGTGTGCTGGACGTCAGGATGGGGGGCCACAGAGGATGGAGGTGAC GCCTCCCCTGTCCTGAACCACGCGGCCGTCCCTTTGATTTCCAACAAGATCTGCAACCACAG GGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG TTAGTGGGAGCGACCAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACAC GAGGAAGGGGACAAGTAGCCACCTGAGTTCCTGAGGTGATGAAGACAGCCCGATCCTCCCCT GGACTCCCGTGTAGGAACCTGCACACGAGCAGACCCCTTGGAGCTCTGAGTTCCGGCACCA GTAGCAGGCCCGAAAGAGGCACCCTTCCATCTGATTCCAGCACAACCTTCAAGCTGCTTTTT GTTTTTTTTTTTTGAGGTGGAGTCTCGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGAAA TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCCTCAGCTTCCCCA GTAGCTGGGACCACAGGTGCCCGCCACCACCCAACTAATTTTTGTATTTTAGTAGAGAC AGGGTTTCACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT CAGCCTCCCACAGTGCTGGGATTACAGGCATGGGCCACCACGCCTAGCCTCACGCTCCTTTC TGATCTTCACTAAGAACAAAGAAGCAGCAACTTGCAAGGGCGGCCTTTCCCACTGGTCCAT CTGGTTTTCTCTCCAGGGTCTTGCAAAATTCCTGACGAGATAAGCAGTTATGTGACCTCACG TGCAAAGCCACCAACAGCCACTCAGAAAAGACGCACCAGCCCAGAAGTGCAGAACTGCAGTC TTTCACATGTGGGGAGGTTAATCTAGGAATGACTCGTTTAAGGCCTATTTTCATGATTTCTT CATTGTCTGGCGTGTCTGCGTGGACTGGTGAATCAAAATCATCCACTGAAA

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><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

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WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVTALHH
SVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT
PLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHR
DVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYT
RVTSFLDWIHEQMERDLKT

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

GCTCAGCGGCGCGCGCGCGCGCGCGCGGGGCTCCGGAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTCGCGA $\texttt{GCCGGCGACG} \underline{\textbf{ATG}} \texttt{GCAGCGCGCCGCTGCCCGTGTCCCCGGCCCGCGCCCTCCTGCTCGCCCTGGCCGGTGCTCT}$ ${\tt GCTCGCGCCCTGCGAGGCCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTCAGTGCCTCTGT}$ CCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGT ACGGGGATATTCTGATTCAGCAGTCAGTCTCAGCACGTGTTCTGGTCTCAGGGGGACTTATTGTGTTTTGAAAATGA AAGCTATGTCTTAGAACCAATGAAAAGTGCAACCAACAGATACAAACTCTTCCCAGCGAAGAAGCTGAAAAGCGT CCGGGGATCATGTGGATCACATCACAACCACCAAACCTCGCTGCAAAGAATGTGTTTCCACCACCCTCTCAGAC ATGGGCAAGAAGGCATAAAAGAGAGACCCTCAAGGCAACTAAGTATGTGGAGCTGGTGATCGTGGCAGACAACCG AGAGTTTCAGAGGCAAGGAAAAGATCTGGAAAAAGTTAAGCAGCGATTAATAGAGATTGCTAATCACGTTGACAA GTTTTACAGACCACTGAACATTCGGATCGTGTTGGTAGGCGTGGAAGTGTGGAATGACATGGACAAATGCTCTGT AAGTCAGGACCCATTCACCAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAAATCCCA TGACAATGCGCAGCTTGTCAGTGGGGTTTATTTCCAAGGGACCACCATCGGCATGGCCCCAATCATGAGCATGTG TGAGCTGGGCCACAATTTCGGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA GGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTTAACCTGCCGGAAGTCAGGGAGTCTTTCGGGGGCCA GAAGTGTGGGAACAGATTTGTGGAAGAAGGAGGAGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTG CTGCAATGCCACCACCTGTACCCTGAAGCCGGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT GAAGCCTGCAGGAACAGCGTGCAGGGACTCCAGCAACTCCTGTGACCTCCCAGAGTTCTGCACAGGGGCCAGCCC TCACTGCCCAGCCAATGTGTACCTGCACGATGGGCACTCATGTCAGGATGTGGACGGCTACTGCTACAATGGCAT CTGCCAGACTCACGAGCAGCAGTGTGTCACGCTCTGGGGACCAGGTGCTAAACCTGCCCCTGGGATCTGCTTTGA GAGAGTCAATTCTGCAGGTGATCCTTATGGCAACTGTGGCAAAGTCTCGAAGAGTTCCTTTGCCAAATGCGAGAT GAGAGATGCTAAATGTGGAAAAATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCATTGGTACCAATGCCGTTTC CATAGAAACAACATCCCTCTGCAGCAAGGAGGCCGGATTCTGTGCCGGGGGACCCACGTGTACTTGGGCGATGA ${\tt CATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAAAATCTGCCTGAATCGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGTCAATGT$ AAATATTAGTGTCTTTGGGGTTCACGAGTGTGCAATGCAGTGCCACGGCAGAGGGGTGTGCAACAACAGGAAGAA CATCCGGCAGCAGCAGCAGGCAGGAGCTGCAGAGTCCAACAGGGAGCGCGGCCAGGGGCCAGGAGCCCGTGGG $\tt CTGCTGCAGAGGGTCACGCGTCCCCAAGGCCTCCTGTGACTGGCAGCATTGACTCTGTGGCTTTGCCATCGTT$ TCCATGACAACAGACACACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCCTACCAGGCACGTCTGCAGAAA CAGTGCAAGGAAGGGCAGCGACTTCCTGGTTGAGCTTCTGCTAAAACATGGACATGCTTCAGTGCTGCTCCTGAG AGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTC $\tt TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTAGCATTTATTATATGAAAAT$ TGAAACAAACTGGAGAAGAAGGTAGGAGAAAGGGCGGTGAACTCTGGCTCTTTGCTGTGGACATGCGTGACCAGC AGTACTCAGGTTTGAGGGTTTGCAGAAAGCCAGGGAACCCACAGAGTCACCAACCCTTCATTTAACAAGTAAGAA TGTTAAAAAGTGAAAACAATGTAAGAGCCTAACTCCATCCCCCGTGGCCATTACTGCATAAAATAGAGTGCATTT GAAAT

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><MW: 80177, pI: 7.08, NX(S/T): 5

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YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLA
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGKDLEKVKQRLIEIANHVDKF
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GGCIMNASTGYPFPMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNRFVEEGEE
CDCGEPEECMNRCCNATTCTLKPDAVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS
PHCPANVYLHDGHSCQDVDGYCYNGICQTHEQQCVTLWGPGAKPAPGICFERVNSAGDPYGN
CGKVSKSSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIETNIPLQQGGRILCRGTHVYLG
DDMPDPGLVLAGTKCADGKICLNRQCQNISVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP
FCDKFGFGGSTDSGPIRQAEARQEAAESNRERGQGQEPVGSQEHASTASLTLI

Signal peptide:

amino acids 1-28

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA
ACAAAACAGTTTTGGGGGTTCAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGA
AGAGGACTCAAAAGTTTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT
GGGCCCAGTGTCCCCTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAAATAGCAGGGTTT
AGTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

CATCCTGCAACATGGTGAAACCACGCCTGGCTAATTTTGTTGTATTTTTGGTAGAGATGGGA TTTCACCGTGTTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCGCCTCGGCCTCCC AAAGTGCTGGGATTACAGGCGAGTGCAACCACCCGGCCACAAACTTTTTAAGAAGTTAAT GAAACCATACCTTTTACATTTTTAATGACAGGAAAATGCTCACAATAATTGTTAACCCAAAA TTCTGGATACAAAGTACAATCTTTACTGTGTAAATACATGTATATGTACTATATGAAAATA TACCAAATATCAATAATACTTATCTCTGGGTAAAAACCTCTTCTCATACCCTGTGCTAACAA CTTTTAACAAAAATTTGCATCACTTTTAAGAATCAAGAAAAATTTCTGAAGGTCATATGGG ACAGAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAAGATTCGAAATCTGCCT TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTTCTAAGCAACTTAAATGTTTTGTTTCGA AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGGAGTGATGTCACTGCCATTATGATGCCCC ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCCAAATGGGTAAGGGGATGGTGGCGA $\mathtt{TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGCAGGTTTCTTCATTTGTT$ CCTTTAACCAGTATGCCGGAAGCTACTGCAGCCGAAACCACAAAGCCCTCCAACAGTGCCCT ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCAT**TAA**GAGG CAGGTCAAGAACAGCTACAGTTCTCCAACCCATACACTAAAACCGAATCCAAATGGTGCCT AGAAGTTCAATGTGGCAAGGAAAAAAACCAGGTCTTCATCAAATCTACTAATTTCACTCCTT GACTAGATGATAAATGCCTGTACTCCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG AGGTCAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA AATATTGACTGGGCGTGGTGAGTGCCTGTGATCCCAGCTACTCAGGTGGCTGAAGCAGG ACAATCACTTGAACTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA CACGCCTGTAATCCCGGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAGGAGATCA AGACCATCCTGGCTAATACAGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCCGGG GATGGTGGCAGCCCTGGAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATAGCGTGAA CTCAGGAGGCGGAGCTTGCAGTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG

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><MW: 6981, pI: 7.47, NX(S/T): 0

 ${\tt MGKGMVAMLILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVVLLAL}$

LHLYH

Signal peptide:

amino acids 15-27

AGGCGGCGGCGGCGGCGGCCGCCCCCCGCGCAGACGGCGAGACGGACAGGACCCGCACAGCAAGCACC TGTACACGGCCGACATGTTCACGCACGGGATCCAGAGCGCCGCGCACTTCGTCATGTTCTTCGCGCCCTGGTGTG GACACTGCCAGCGGCTGCAGCCGACTTGGAATGACCTGGGAGACAAATACAACAGCATGGAAGATGCCAAAGTCT ${\tt ATGTGGCTAAAGTGGACTGCACGGCCCACTCCGACGTGTGCTCCGCCCAGGGGGTGCGAGGATACCCCACCTTAA}$ GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAAGGCGACCACTTTATCAAGTTCTTCGCTC $\tt CGTGGTGTGGTCACTGCAAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCTTGAACATTCCGAAACTG$ ${\tt TCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACTCTGCTCCGGAAACCAGGTTCGTGGCTATCCCACTC}$ TTCTCTGGTTCCGAGATGGGAAAAAGGTGGATCAGTACAAGGGAAAGCGGGATTTGGAGTCACTGAGGGAGTACG TGGAGTCGCAGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTCACGCCCTCAGAGGCCCCGGTGCTGGCAG TAACCTTCATCAAGTTTTATGCTCCATGGTGTGGTCATTGTAAGACTCTGGCTCCTACTTGGGAGGAACTCTCTA AAAAGGAATTCCCTGGTCTGGCGGGGGTCAAGATCGCCGAAGTAGACTGCACTGCACCGGAATATCTGCAGCAAGTATTCGGTACGAGGCTACCCCACGTTATTGCTTTTCCGAGGAGGAAGAAAGTCAGTGAGCACAGTGGAGGCA ${\tt GAGACCTTGACTCGTTACACCGCTTTGTCCTGAGCCAAGCGAAAGACGAACTT} \underline{{\tt TAG}} {\tt GAACACAGTTGGAGGTCAC}$ $\tt CTCTCCTGCCCAGCTCCGCACCCTGCGTTTAGGAGTTCAGTCCCACAGAGGCCACTGGGTTCCCAGTGGTGGCT$ ATTCTTTATTAAGTTAAGTTTCTCTAAGTAAATGTGTAACTCATGGTCACTGTGTAAACATTTTCAGTGGCGATA TATCCCCTTTGACCTTCTCTTGATGAAATTTACATGGTTTCCTTTGAGACTAAAATAGCGTTGAGGGAAATGAAA ${\tt CCACGAGTTCTGGAAAGGTGGCCTTGTGGCAGTATTGACGTTCCTCTGATCTTAAGGTCACAGTTGACTCAATAC}$ ${\tt TGTGTTGGTCGTAGCATGGAGCAGATTGAAATGCAAAAACCCACACCTCTGGAAGATACCTTCACGGCCGCTGC}$ TGGAGCTTCTGTTGCTGTGAATACTTCTCTCAGTGTGAGAGGGTTAGCCGTGATGAAAGCAGCGTTACTTCTGACC GTGCCTGAGTAAGAGAATGCTGATGCCATAACTTTATGTGTCGATACTTGTCAAATCAGTTACTGTTCAGGGGAT $\tt CCTTCTGTTTCTCACGGGGTGAAACATGTCTTTAGTTCCTCATGTTAACACGAAGCCAGAGCCCACATGAACTGT$ TGGATGTCTTCCTTAGAAAGGGTAGGCATGGAAAATTCCACGAGGCTCATTCTCAGTATCTCATTAACTCATTGA AAGATTCCAGTTGTATTTGTCACCTGGGGTGACAAGACCAGACAGGCTTTCCCAGGCCTGGGTATCCAGGGAGGC TCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTCTGATTCTGTTTCTCAGTAGTCCTTTTAGAGG $\tt CTTGCTATACTTGGTCTGCTTCAAGGAGGTCGACCTTCTAATGTATGAAGAATGGGATGCATTTGATCTCAAGAC$ CAAAGACAGATGTCAGTGGGCTGCTCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGTCCTCTA ACTCATGCTGTCCTTGTGATTAAACACCTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAAGCTCTAAGATA $\tt CCCATACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACTGGTGGTAGGAATCTTAGAAACAAGACCACTTATA$ CTGTCTGTCTGAGGCAGAAGATAACAGCAGCATCTCGACCAGCCTCTGCCTTAAAGGAAATCTTTATTAATCACG TATGGTTCACAGATAATTCTTTTTTAAAAAAACCCAACCTCCTAGAGAAGCACAACTGTCAAGAGTCTTGTACA GATACTTTCTAAATAAACTCTTTTTTTTAA

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><subunit 1 of 1, 432 aa, 1 stop

><MW: 47629, pI: 5.90, NX(S/T): 0

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SDVCSAQGVRGYPTLKLFKPGQEAVKYQGPRDFQTLENWMLQTLNEEPVTPEPEVEPPSAPE
LKQGLYELSASNFELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT
QHYELCSGNQVRGYPTLLWFRDGKKVDQYKGKRDLESLREYVESQLQRTETGATETVTPSEA
PVLAAEPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL

Signal sequence:

amino acids 1-32

CTTTTCTGAGGAACCACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA CCGCTGAAGTCTGTGCCACACACACAATTTCACCAGGACCCAAAGGAGATGATGGTGAAAAA GGAGATCCAGGAGAAGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTGGGAAGA AGGGTGACAAAGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACTGGATATTAGTATTGCTCGGCT CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAAT TCTACTACATCGTGCAGGAAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGG GGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACTCATCGCTGACTATGTTGC TGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC CCCTATGGTCATGAGGACTGTGTGGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAG**TAA**CTTCCCTCATCCT ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT CCATCATCAAAAAAAAAAAAAAA

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980</pre>

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

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Signal peptide:

amino acids 1-25

GGTTCTATCGATTCGAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC GCCAGCGCACGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTT CGGAAGGGAGGATCAGGGATGTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGC AGCTACACCTCTGGCCGCAGTTGCGCTGGCTTCCGGCGGACTTGGCCTTTGCGGTGCGAGCT CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCGACCCGGAAGG ACACCTTTCTCATTCACGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC AGGGCTGCACGCGCCTTCCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCGGCGACAG CGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGCAGCCGGGGAGCCGGAGATGCAGCGGCCG GAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGCCGCCAGAGGTGGAGGAGCCGCCGCCCCT CTGTCACCTGGAGCAACTGTGGCGCTGCTCCTCCCGGTGGCCCAGAGTTTCTGTGGCTCTG GTTCGGGCTGGCCAAGGCCGGCCTGCGCACTGCCTTTGTGCCCACCGCCCTGCGCCGGGGCC GAGTCCCTGGAGCCGGACCTGCCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGG GGCCAGTGCCAGGATACCTCTCTCCCCCCAGAGCATAACAGACACGTGCCTGTACATCTTC ACCTCTGGCACCACGGGCCTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG CCAGGGCTTCTATCAGCTGTGTGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCCAC TCTACCACATGTCCGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCCATTGGGGCCACAGTG GTGCTGAAATCCAAGTTCTCGGCTGGTCAGTTCTGGGAAGATTGCCAGCAGCACAGGGTGAC GGTGTTCCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACCAGCCCCCGAGCAAGGCAG AACGTGGCCATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCCAGATACCTGGGAGCGT TTTGTGCGGCCCTTCGGGCCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT GGCCACCATCAACTACACAGGACAGCGGGGCGCTGTGGGGCGTGCTTCCTGGCTTTACAAGC ATATCTTCCCCTTCCTTGATTCGCTATGATGTCACCACAGGAGAGCCAATTCGGGACCCC CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCA GCAGTCCCCATTCCTGGGCTATGCTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGG ATGTCTTCCGGCCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC CACAACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATG GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCCC CACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCACCTTATGCCCG GCCCCGATTCCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAG TTCGGATGGCAAATGAGGGCTTCGACCCCAGCACCCTGTCTGACCCCACTGTACGTTCTGGAC CAGGCTGTAGGTGCCTACCTGCCCTCACAACTGCCCGGTACAGCGCCCCTCCTGGCAGGAAA CCTTCGAATC**TGA**GAACTTCCACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGGTGGGG CCGTTGCAGGTGTACTGGGCTGTCAGGGATCTTTTCTATACCAGAACTGCGGTCACTATTTT AAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGC TTGGCCGCCATGGCCCAACTTGTTTATTGCAG

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><MW: 78644, pI: 7.65, NX(S/T): 2

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RAAHTFLIHGSRRFSYSEAERESNRAARAFLRALGWDWGPDGGDSGEGSAGEGERAAPGAGD
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGLAKAGLRTAFVPTAL
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA
EVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL
ALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP
SKAERGHKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW
LYKHIFPFSLIRYDVTTGEPIRDPQGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPELAQGK
LLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEV
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPPYARPRFLRLQESLATTETFK
QQKVRMANEGFDPSTLSDPLYVLDOAVGAYLPLTTARYSALLAGNLRI

Type II transmembrane domain:

amino acids 45-65

Other transmembrane domain:

amino acids 379-398

cAMP- and cGMP-dependent protein kinase phosphorylation site starting at amino acid 136

CUB domain protein motif

amino acids 254-261

putative AMP-binding domain siganture

amino acids 332-343

N-glycosylation sites

amino acids 37-40 and 483-486

CCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA GCTTGTCCATCTCCCTCCCGGGGGAGCCGCGCGCGCCTCCCACCTTTGCCGCACACTCCGGC GAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGAACTCGGATTGCAGCTCTGAACCC CCATGGTGGTTTTTAAACACTTCTTTTCCTTCTCTCTCGTTTTGATTGCACCGTTTCCA CCATCTGGCTTATAAAAGTTTGCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCCTCGG CTGGCAGAAGGGGGTGACGCTGGGCAGCGCGAGGAGCGCGCCGCTGCCTCTGGCGGGCTTT CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCCGTGGGGTTTACCGAGCTGGATTTGTATG TTGCACCATGCCTTCTTGGATCGGGGCTGTGATTCTTCCCCTCTTGGGGCTGCTGCTCTCCC TCCCCGCCGGGGCGATGTGAAGGCTCGGAGCTGCGAGAGGTCCGCCAGGCGTACGGTGCC AAGGGATTCAGCCTGGCGGACATCCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTG TCCTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAGCAAAC TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCCAGG CATAAGAAATTTGACGAATTTTTCCGAGAGCTCCTGGAGAATGCAGAAAAGTCACTAAATGA TATGTTTGTACGGACCTATGCATGCTGTACATGCAGAATTCAGAAGTCTTCCAGGACCTCT TCACAGAGCTGAAAAGGTACTACACTGGGGGTAATGTGAATCTGGAGGAAATGCTCAATGAC TTTTGGGCTCGGCTCCTGGAACGGATGTTTCAGCTGATAAACCCTCAGTATCACTTCAGTGA AGACTACCTGGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTTGGAGACGTGCCCC GGAAACTGAAGATTCAGGTTACCCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTG ACTGTGGGCAGAGATTGCAAACCGAGTTTCCAAGGTCAGCCCAACCCCAGGGTGTATCCG TGCCCTCATGAAGATGCTGTACTGCCCATACTGTCGGGGGCTTCCCACTGTGAGGCCCTGCA ACAACTACTGTCTCAACGTCATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG TGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACAT TGAGTCGGTCATGGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAA ACAGCATGCAGGTGTCTGCAAAGGTCTTTCAGGGATGTGGTCAGCCCAAACCTGCTCCAGCC CTCAGATCTGCCCGCTCAGCTCCTGAAAATTTTAATACACGTTTCAGGCCCTACAATCCTGA GGAAAGACCAACAACTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGACATAAAAGAGA AATTGAAGCTCTCTAAAAAGGTCTGGTCAGCATTACCCTACACTATCTGCAAGGACGAGAGC GTGACAGCGGGCACGTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT GCCTGAGATCATGAATGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACA TCACTCGGCCTGACACTTTCATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAA CTAAAAAACGCCTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG CTCAGGGAGTGGCAGTGGATGACGTGTGTCCCACGGAGTTTGAGTTTGTCACCA CAGAGGCCCCCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCCAGCGTGGC CACTCCCTGCTCTCGGTCTCTCACCTGCATTGTCCTGGCACTGCAGAGACTGTGCAGA ${f A}$ TCTTGGGTTTTTGGTCAGATGAAACTGCATTTTAGCTATCTGAATGGCCAACTCACTTCTT TTCTTACACTCTTGGACAATGGACCATGCCACAAAAACTTACCGTTTTCTATGAGAAGAGAG CAGTAATGCAATCTGCCTCCCTTTTTGTTTTCCCAAAGAGTACCGGGTGCCAGACTGAACTG CTTCCTCTTTCCTTCAGCTATCTGTGGGGACCTTGTTTATTCTAGAGAGAATTCTTACTCAA ATTTTTCGTACCAGGAGATTTTCTTACCTTCATTTGCTTTATGCTGCAGAAGTAAAGGAAT CTCACGTTGTGAGGGTTTTTTTTTTTTCTCATTTAAAAT

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><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

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EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKSLNDMF
VRTYGMLYMQNSEVFQDLFTELKRYYTGGNVNLEEMLNDFWARLLERMFQLINPQYHFSEDY
LECVSKYTDQLKPFGDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAERLEGPFNIES
VMDPIDVKISEAIMNMQENSMQVSAKVFQGCGQPKPAPALRSARSAPENFNTRFRPYNPEER
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGHSKARYLPE
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG
SGSGCMDDVCPTEFEFVTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

Signal peptide:

amino acids 1-23

FIGURE 42A

CGGACGCGTGGGCGGCGCGCGAAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAACGCACG CAGTTTGCAGCGCCTGCGCCGGGTGCGCCAACTACGCAAAGACCAAGCGGGCTCCGCGCGGACCGGCCGCGGGGC TAGGGACCCGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT GGAGGGAGATCAGGAAACGGCTTCTTCCTCACTTCGCCGCCTGGTGAGTGTCGGGGAGATTGGCAAACGCCTAGG AAAGGACTGGGGAAAATAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCCGGTCCACTACGGCAGTTTATCTG TCTGATCAGAGCCAGACGCGACGCGTCCACTTCGCAGTTCTTTCCAGGTGTGGGGACCGCAGGACAGACGGCCGA TCCCGCCGCCTCCGTACCAGCACTCCCAGGAGAGTCAGCCTCGCTCCCCAACGTCGAGGGCGCTCTGGCCACGA CGGACATGGTGACAGCTGAGAGGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTCACCGTCTGTTGGGTGCATG TGTGCGCCCGCAGCGGCGCGGGGCGCGTGGTTCTCCGCGTGGAGTCTCACCTGGGACCTGAGTGA**ATG**GCTCCCA CGCTGGCAGGATTCTGGATCCTCTGCCTCCTCACTTATGGTTACCTGTCCTGGGGCCCAGGCCTTAGAAGAGGAGG AAGAAGGGGCCTTACTAGCTCAAGCTGGAGAGAAACTAGAGCCCAGCACAACTTCCACCTCCCAGCCCCATCTCA TTTTCATCCTAGCGGATGATCAGGGATTTAGAGATGTGGGTTACCACGGATCTGAGATTAAAACACCTACTCTTG ACAAGCTCGCTGCCGAAGGAGTTAAACTGGAGAACTACTATGTCCAGCCTATTTGCACACCATCCAGGAGTCAGT TTATTACTGGAAAGTATCAGATACACACCGGACTTCAACATTCTATCATAAGACCTACCCAACCCAACTGTTTAC TGGGTTTTAACAGAAAAGAATGCATGCCCACCAGAAGAGGATTTGATACCTTTTTTGGTTCCCTTTTTGGGAAGTG GGGATTACTATACACACTACAAATGTGACAGTCCTGGGATGTGTGGCTATGACTTGTATGAAAACGACAATGCTG CCTGGGACTATGACAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTTAGCTTCCCATA TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTTCCTGCTTAGATGAAGCAA TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTCTATAACAACAGCATTATCATTTACTCTTCAGATAATG GTGGCCAGCCTACGGCAGGAGGAGTAACTGGCCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC GGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTAAGGAACTTGTGCACATCACTG ACTGGTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT GGGAGACCATAAGTGAGGGTCTTCGCTCACCCCGAGTAGATATTTTGCATAACATTGACCCCTATACACCAAGGC AAAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG GAAATTGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCCCTCAGTCTTTCAGCAACCTGGGACCGAACCG GTGGCACAATGAACGGATCACCTTGTCAACTGGCAAAAGTGTATGGCTTTTCAACATCACAGCCGACCCATATGA GAGGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCACAGTTCAACAAAAC TGCAGTGCCGGTCAGGTATCCCCCCAAAGACCCCAGAAGTAACCCTAGGCTCAATGGAGGGGTCTGGGGACCATG GAAGAAGAACAGCAGAAAGCAGTCTCAGGTAAACCAGCAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA GGCTTGTTTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCACACTGAAAACTGTCCTGCTCAGTG CCAAGGTGCTACTCTTGCAAGCCACACTTAGAGAGAGTGGAGATGTTTATTTCTCTCGCTCCTTTAGAAAACGTG GTGAGTCCTGAGTTCCACTGCTGTGCTTCAGTCAACTGACCAAACACTGCTTTGAATTATAGGAGGAGAACAATA ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAAAACTACCTTTGATAAATTAC

FIGURE 42B

CACTTGGGTTTTTTAATTAATTCTATTTTATATATATAAATATATGTTTCTTTTCCTGTGAAAAGCTGTTTTTCT CACATGTGAACAGCTTGCACCTCATTTTACCATGCGTGAGGGAATGGCAAATAAGAATGTTTGAGCACACTGCCC GAAAAATATTTTGTTGTTTTTATAAAAAGTTATGCAAATGACTTTTATTTTATTTTCCTGCATACCATTAGAAGA ATTTTATTTCATTCTTCAAATTATCAAGCACTGTAATACTATAAATTAATGTAATACTGTGTGAATTCAGACTA ATTACTTGGAAATTCAATGTTTGTGCAGAGTTGAGACAACTTTATTGTTTCTATCATAAACTATTTATGTATCTT AATTATTAAAATGATTTACTTTATGGCACTAGAAAATTTACTGTGGCTTTTCTGATCTAACTTCTAGCTAAAATT GTATCATTGGTCCTAAAAAATAAAAATCTTTACTAATAGGCAATTGAAGGAATGGTTTGCTAACAACCACAGTAA TATAATATGATTTTACAGATAGATGCTTCCCCTTGGCTATGACATGGAGAAAGATTTTCCCATAATAATAACTAA TATTTATATTAGGTTGGTGCAAAACTAGTTGCGGTTTTTCCCATTAAAAGTAATAACCTTACTCTTATACAAAGT ACATGCAAACGTCATGAGGAGAATTAAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTCATCAATGAGCATA GATTGGTGTGGATCCTGTAGACCCTGGTGTTTTCTTTGAAGTGCCCTCTCCTAATGCAGAGGCCTTGAAGCTTAC AGTATACACTTGAAAAGTCACAGATAGCTAGAATTATGATCTTTGAAGTTATAACTGTGATCTGAAAATGTGTGT GGTGGTATGACAGCATACCATTAAATACATTTACATCACAGCTCAAAGGACTGTGATATAATCCATTTATATCAC AACTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAATGTATAAAAGAATCTATAAT CTAGTACTGAAATTACTAAATTGGGTAAGATGATTTAAATGATTTTAATTTTAACATTTTATTTCTAGAATATAT GGCTCCATTTTATTTTATAGTGTAAAGTTGTATTTCCTAAAGTTTGTGTTTTTGTCGACAGTATCTTTTAAATGAG

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><subunit 1 of 1, 515 aa, 1 stop

><MW: 56885, pI: 6.49, NX(S/T): 5

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GEKLEPSTTSTSQPHLIFILADDQGFRDVGYHGSEIKTPTLDKLAAEGVKLENYYVQPICTP
SRSQFITGKYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVGYSTHMVGKWHLGFNRKEC
MPTRRGFDTFFGSLLGSGDYYTHYKCDSPGMCGYDLYENDNAAWDYDNGIYSTQMYTQRVQQ
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLDEAINNVTLA
LKTYGFYNNSIIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGFVHSPLLKNKGTVCK
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG
QQAMGSGTLQSSQPSECSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGFS
TSQPTHMRGWTYLTGIQES

Important Features:

Signal Peptide:

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC CCGTGCGAGATGCCTCTGCCCTGGAGCCTTGCGCTCCCGCTGCTGCTCTCCTGGGTGGCAG GTGGTTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTTGTTAGCATCGGCACGTCAGCCT GGGGTCTGTCACTATGGAACTAAACTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG GCAGATGCTTTCCAGGATACACCGGGAAAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG AAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGCTTTTGCCT CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGAACTCTAGGACATGTGCCATGATAA ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGA CTCCGCCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAAATGTCACA ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCCTTCAAGTG TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTTCTGCTATCCCTGAAAATTCTG AAAAACAGCATGAAAAAGAAGGCAAAAATTAAAAATGTTACCCCAGAACCCACCAGGACTCC TACCCCTAAGGTGAACTTGCAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAACT CTCATGGAGGTAAAAAAGGGAATGAAGAGAAA**TGA**AAGAGGGGCTTGAGGATGAGAAAGAG AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTTTTTTCCCT AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAACTTCCAA ACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACT GGAAACAGGATAGAGAAGATGATTTTGACTGGAATCCTGCTGATCGAGATAATGCTATTGGC CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG ACAAAGTCGGGAAACTTCGAGTGTTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAG ACCACGAGTGAGGATGAAAAGTGGAAGACAGGGAAAATTCAGTTGTATCAAGGAACTGATGC TACCAAAAGCATCATTTTTGAAGCAGAACGTGGCAAGGGCCAAAACCGGCGAAATCGCAGTGG ATGGCGTCTTGCTTGTTTCAGGCTTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG TTACTATCTTTATATTTGACTTTGTATGTCAGTTCCCTGGTTTTTTTGATATTGCATCATAG GACCTCTGGCATTTTAGAATTACTAGCTGAAAAATTGTAATGTACCAACAGAAATATTATTG TAAGATGCCTTTCTTGTATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT TCTCAGTCATTTCTGAATCTTTCCNCATTATATTATAAAATNTGGAAANGTCAGTTTATCTC CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTTCTA GAAAATAGAAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGGA AACTATGACATCAAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC TTGTATATTTAATTCTTTGTAATAATAA

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCE
ATCEPGCKFGECVGPNKCRCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGSYKCFCLSGH
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP
YNRRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPTPK
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

Signal peptide:

amino acids 1-21

EGF-like domain cysteine pattern signature.

amino acids 80-91

Calcium-binding EGF-like domains

amino acids 103-124, 230-251 and 185-206

GGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTCCTGCTCTTGGTGCAGCTGCTG CGCTTCCTGAGGGCTGACGCCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCC AGAATGGGAGCTGACTGAT**ATG**GTGGTGTGGGTGACTGGAGCCTCGAGTGGAATTGGTGAGG AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGTGCTGTCAGCCAGAAGAGTGCAT GAGCTGGAAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAAGATATACT TGTTTTGCCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAATGTCCCAGCGTTCTCTGTGC ATGGATACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTC CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA CTCCGGGGTTTTTTTAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC ${ t TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAGTCA}$ CAAAGACTATAGGCAATAATGGAGACCAGTCCCACAAGATGACAACCAGTCGTTGTGTGCGG CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGGATCTCAGAACAACCTTTCTT GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG GGAAGAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAAATC GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT ATTGCCATGAATCTTGCAAAA

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><subunit 1 of 1, 289 aa, 1 stop

><MW: 32268, pI: 9.21, NX(S/T): 0

MVVWVTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPLDL TDTGSHEAATKAVLQEFGRIDILVNNGGMSQRSLCMDTSLDVYRKLIELNYLGTVSLTKCVL PHMIERKQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGP VQSNIVENSLAGEVTKTIGNNGDQSHKMTTSRCVRLMLISMANDLKEVWISEQPFLLVTYLW QYMPTWAWWITNKMGKKRIENFKSGVDADSSYFKIFKTKHD

Important Features:

Signal Peptide:

amino acids 1-31

Transmembrane domain:

amino acids 136-157

Tyrosine kinase phosphorylation site.

106-113 and 107-114

Homologous region to Short-chain alcohol dehydrogenase

amino acids 80-90, 131-168, 1-13 and 176-185

GCGACGTGGGCACCGCCATCAGCTGTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGTTTC TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGCCTCTGTCC TGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTC TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCCAGGGCAAGGCTAAGAGGCACTGAGCCCTCA ACCCAAGCCAGGCTGACCTCATCTGCTTTGCTTTCAAGCCGCTCAGCGTGCCTGTG GACAGCGTGGCCCCGGCCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC CTGGGTCCTCACTGCTGCCCACTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGGT CAGTGGTCCTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG GCTGCCCTGCAGTTGCCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGCTCCTGGGACC CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACTGTATCTACAACCAGCT GCACCAGCGACACCTGTCCAACCCGGCCCGGCCTGGGATGCTATGTGGGGGCCCCCAGCCTG GGGTGCAGGGCCCCTGTCAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGA CACTGGGTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGT GCTGCTGACCAACACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCCAGCTT TCCTGGCCCAGAGCCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCCTCCCCATGGCCCTGGGAGGCCAGGCT GATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTCAGAGGAGGCGGTGCTAACTG CTGCCCACTGCTTCATTGGGCGCCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGA TCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG GCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAG GGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG TGTGTACCAGTGCTGTGGGTGAGCTGCCCAGCTGTGAGGGCCTGTCTGGGGCACCACTGGTG CATGAGGTGAGGGCACATGGTTCCTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG CCCCGCCAGGCCGGCGTCTTCACCGCGCTCCCTGCCTATGAGGACTGGGTCAGCAGTTTGG ACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCGAGGCTGAGCCTGGAAGCTGCCTGGCC AACATAAGCCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC AGGCAGGCAAATGGCATTACTGCCCCTGTCCTCCCCACCCTGTCATGTGATTCCAGGCAC CTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCCACACCCCAACTCTGCTACCAAGC AAAATAAAA

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MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV
PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGA
EEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTS
DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLC
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEMSDEDS
CVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSV
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGERG
WVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTSAVGELPSCEGLS
GAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEP
GSCLANISOPTSC

Important features:

Signal peptide:

amino acids 1-15

Homologous region to Serine proteases, trypsin family amino acids 79-95, 343-359 and 237-247

N-glycosylation sites.

amino acids 37-40 and 564-567

Kringle domains

amino acids 79-96, 343-360 and 235-247

CGGGCCGCCCCGGCCCCATTCGGGCCGGGCCTCGCTGCGGCGGCGACTGAGCCAGGCTGG GCCGCGTCCCTGAGTCCCAGAGTCGGCGCGCGCGCGCAGGGCCAGCCTTCCACCACGGGGAG CCCAGCTGTCAGCCGCCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGT GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTCCC ${\tt CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACA}$ GCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC GACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGGGATTTCGGCAGCGCTGCCGTCAGCCT GCAGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTC TGGCAGGATGGCCAGGTGTGCCCCTGACTGGCAACGTGACCACGTCGCAGATGGCCAACGA GCAGGGCTTGTTTGATGTGCACAGCGTCCTGCGGGTGGTGCTGGGTGCGAATGGCACCTACA GCTGCCTGGTGCGCAACCCCGTGCTGCAGCAGGATGCGCACRGCTCTGTCACCATCACAGGG TGCACTGCTGGTGGCCCTGGCTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGAGAAGGCTCCAAGACAGCCCTGCAGCCT CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCC**TGA**CCATGAGGACCAGG GAGCTGCTACCCCTCCCTACAGCTCCTACCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC TGCCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTT GCCTTATTTCACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCTC TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTCAGA CTGACTGACCCCTGCCTTATTTCACCAAAGACACGATGCATAGTCACCCCGGCCTTGTTTC TCCAATGGCCGTGATACACTAGTGATCATGTTCAGCCCTGCTTCCACCTGCATAGAATCTTT ${\tt TCTTCTCAGACAGGGACAGTGCGGCCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCCTTTC}$ CCCTCCTTCCTCCCTGCCCCAAGTGAAGACAGGGCCAGGGCCAGGAATGCTTTGGGGACACCG AGGGGACTGCCCCCCCCCCCCCCCTGGTGCTATTCTGGGGCTGGGGCAGTCTTTTCCTGGC TTGCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG GATGTCATCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC AAAAAAAAAAA

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><subunit 1 of 1, 316 aa, 1 stop, 1 unknown

><MW: -1, pI: 4.62, NX(S/T): 4

MLRRRGSPGMGVHVGAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPEPGFSLAQ
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQGVPL
TGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA
LWVTVGLSVCLIALLVALAFVCWRKIKQSCEEENAGAEDQDGEGEGSKTALQPLKHSDSKED
DGQEIA

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC amino acids 217-234

TTCGTGACCCTTGAGAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC CTGAACTTGTCTGAAGCCCTTGTCCGTAAGCCTTGAACTACGTTCTTAAATCTATGAAGTCG AGGGACCTTTCGCTGCTTTTGTAGGGACTTCTTTCCTTGCTTCAGCAAC**ATG**AGGCTTTTCT TGTGGAACGCGGTCTTGACTCTGTTCGTCACTTCTTTGATTGGGGCTTTGATCCCTGAACCA GAAGTGAAAATTGAAGTTCTCCAGAAGCCATTCATCTGCCATCGCAAGACCAAAGGAGGGGGA TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC ACAAACATAACAATGGTCAGCCCATTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT TGGGACCAGGGCTTGAAAGGAATGTGTGTAGGAGAGAAGAAAAGCTCATCATTCCTCCTGC TCTGGGCTATGGAAAAGAAGGAAAAGGTAAAATTCCCCCAGAAAGTACACTGATATTTAATA TTGATCTCCTGGAGATTCGAAATGGACCAAGATCCCATGAATCATTCCAAGAAATGGATCTT AATGATGACTGGAAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA ACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTGATAAAG AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA TAGAGATACATCTACCCTTTTAATATAGCACTCATCTTTCAAGAGAGGGCCAGTCATCTTTAA GGGAAGAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTTCACTTTCACAG ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAAATGTTGCAACTGGGAATATACC ACGACATGAGACCAGGTTATAGCACAAATTAGCACCCTATATTTCTGCTTCCCTCTATTTTC TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT GTTATAATGAAATAGTTTATGTGTAACTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA TGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAG GCTGAGGCGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA CCCTATCTCTACTAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCCTGTAATCCCAGCT ACCCAGGAAGGCTGAGGCGGCAGAATCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAG ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGGCTCCTAGTGAT TGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATG TATCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGC TAGCGGAATATCCTTCCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA TTGTATCATAAGATAAAGTAGTAAACCAGTCTACATTTTCCCATTTCTGTCTCAAAAAAC TGAAGTTAGCTGGGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGGGCCCAAGGAGGG TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTA CTAAAAATACAAAAATTAGCCAGGCGTGGTGGTGCACACCTGTAGTCCCAGCTACTCGGGAG GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCC CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATTTT

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><subunit 1 of 1, 211 aa, 1 stop

><MW: 24172, pI: 5.99, NX(S/T): 1

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Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

CCAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCCTCTCCCGTAGCCCACCCGA CTAACATCTCAGTCTCTGAAA**ATG**CACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT CACGGGGCTCAGTCTCTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTAC CTGCCACCTCAACGTCCTCAATGGCTCTGACGCCCGGCTGCCCTGCACCTTCAACTCCTGC TACACAGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACTGCTC TGAGGAGATGTTCCTCCAGTTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAG ACCGCGTGGAGTTCTCAGGGAACCCCAGCAAGTACGATGTGTCGGTGATGCTGAGAAACGTG CAGCCGGAGGATGAGGGGATTTACAACTGCTACATCATGAACCCCCCTGACCGCCACCGTGG CCATGGCAAGATCCATCTGCAGGTCCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG CCGTGATTGTGGGTGCCTCCGTCGGGGGCTTCCTGGCTGTTGGTCATCTTGGTGCTGATGGTG GTCAAGTGTGTGAGGAGAAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA GGAGGCCAAGACGGACGGTGAAGGCAACCCGGATGATGGCGCCAAG**TAG**TGGGTGGCCGGCC CTCTTGGTGTGCTTCCCGTGACCTAGGACCCCAGGGCCCACCTGGGGCCTCCTGAACCCCCG ACTTCGTATCTCCCACCCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA TGCTCTGGGACGTGTGGGCCCTGGGGAGAGAGAGAAAGGGCTCCCACCTGCCAGTCCCTGG GGAGGGGCCGCTGTCACCTGCCCAGTGCTTGCCTGGCAGTGGCTTCAGAGAGGACCTGGTGG GGAGGGAGGGCTTTCCTGTGCTGACAGCGCTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTG TGCTCCTCCCTGCTCCCAGCCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCCTGA AACTTGGAGGGCATGTTAAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGG CTGCAGGCAAAGCTGGACATGTGCCCTGGCCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCCAGCGGGGACCCACCAACAGAGGCC AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGCTCCATGGTGAATGCAGGTTGCTGCAG GCTCTGCCTTCTCCATGGGGTAACCACCCTCGCCTGGGCAGGGCAGCCAAGGCTGGGAAAT GAGGAGGCCATGCACAGGGTGGGGCAGCTTTCTTTGGGGCTTCAGTGAGAACTCTCCCAGTT GCCCTTGGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGAAAGGCGAAAGCCTGAGGCCG GCATAAGGGGAGGCCTTGGAACCTGAGCTGCCAATGCCAGCCCTGTCCCATCTGCGGCCACG CTACTCGCTCCCCAACAACTCCCTTCGTGGGGACAAAAGTGACAATTGTAGGCCAGGC ACAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCCAAGGCGGGTGGATTACCTCCAT CTGTTTAGTAGAAATGGGCAAAACCCCATCTCTACTAAAAATACAAGAATTAGCTGGGCGTG GTGGCGTGTGCCTGTAATCCCAGCTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG GGAAGCAGAGGTTGCAGTGAACTGAGATAGTGATAGTGCCACTGCAATTCAGCCTGGGTGAC ATAGAGAGACTCCATCTCAAAAAAAA

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<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

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Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTT
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC
TCAATGGCTCTGACGCCCGCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC
AGTTCTCCTGAACTGGACTTACCAGGAGTGCAACAACTGCTCTGAGGAGATGTTCCTCCAG
TTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG
GAACCCCAGCAAGTACGATGTCCGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA
TTTACAACTGCTACATCATGAACCCCCC

 ${\tt TGCGGCGACCGTCGTACACCATGGGCCTCCACCTCCGCCCCTACCGTGTGGGGCTGCTCCCGGATGGCCTCCTGT}$ CTGGTGATTTGGGTAACCAACTGGAAGCCAAGCTGGACAAGCCGACAGTGGTGCACTACCTCTGCTCCAAGAAGA CCGAAAGCTACTTCACAATCTGGCTGAACCTGGAACTGCTGCTGCTGTCATCATTGACTGCTGGATTGACAATA TCAGGCTGGTTTACAACAAAACATCCAGGGCCACCCAGTTTCCTGATGGTGTGGATGTACGTGTCCCTGGCTTTG GGAAGACCTTCTCACTGGAGTTCCTGGACCCCAGCAAAAGCAGCGTGGGTTCCTATTTCCACACCATGGTGGAGA GCCTTGTGGGCTGGGGCTACACACGGGGTGAGGATGTCCGAGGGGCTCCCTATGACTGGCGCCGAGCCCCAAATG AAAACGGGCCCTACTTCCTGGCCCTCCGCGAGATGATCGAGGAGATGTACCAGCTGTATGGGGGCCCCGTGGTGC TGGTTGCCCACAGTATGGGCAACATGTACACGCTCTACTTTCTGCAGCGGCAGCCGCAGGCCTGGAAGGACAAGT ACAACAACCGGATCCCAGTCATCGGGCCCCTGAAGATCCGGGAGCAGCGGTCAGCTGTCTCCACCAGCTGGC TGCTGCCCTACAACTACACATGGTCACCTGAGAAGGTGTTCGTGCAGACACCCACAATCAACTACACACTGCGGG ${\tt AAGCCACGATGCCACCTGGCGTGCAGCTGCACTGCCTCTATGGTACTGGCGTCCCCACACCAGACTCCTTCTACT}$ ATGAGAGCTTCCCTGACCGTGACCCTAAAATCTGCTTTGGTGACGGCGATGGTACTGTGAACTTGAAGAGTGCCC TGCAGTGCCAGGCCTGGCAGAGCCGCCAGGAGCACCAAGTGTTGCTGCAGGAGCTGCCAGGCAGCGAGCACATCG $AGATGCTGGCCAACGCCACCACCCTGGCCTATCTGAAACGTGTGCTCCTTGGGCCC\underline{TGA}CTCCTGTGCCACAGGA$ CTCCTGTGGCTCGGCCGTGGACCTGCTGTTGGCCTCTGGGGCTGTCATGGCCCACGCGTTTTTGCAAAGTTTGTGA GTGGCAGTGAAGAAGAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAATGCTGCTGATGGTGGA TGTCCCCCTATTCCTGTGGGCTTTTCATACTTGCCTACTGGGCCCTGGCCCCGCAGCCTTCCTATGAGGGATGTT ${\tt GCCACAGATAGGCCTGCCACTGGTCATGGGTAGCTAGAGCTGCTGGCTTCCCTGTGGCTTAGCTGGTCGCCAGCCCCTGTGGCTAGCTGGTCAGGCCAGCCCAGCCCCAGCCCAGGCCAGCCCAGCCCAGCCCAGGCCAGCCCAGGCCAGCCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAG$ $\tt CCTGGGACATCTCACTCCACTCCCTTACCACCAGGAGCATTCAAGCTCTGGATTGGGCAGCAGATGTG$ $\tt CCCCCAGTCCCGCAGGCTGTGTTCCAGGGGCCCTGATTTCCTCGGATGTGCTATTGGCCCCAGGACTGAAGCTGC$ GAAAGGGAATCCAAGGAAGCAGCCAAGGCTGCTCGCAGCTTCCCTGAGCTGCACCTCTTGCTAACCCCACCATCA $\tt CCTGGCCAGCACCCAGCTTAGTGCTGGGACTAGCCCAGAAACTTGAATGGGACCCTGAGAGAGCCAGGGGTCCCC$ TGAGGCCCCCTAGGGGCTTTCTGTCTGCCCCAGGGTGCTCCATGGATCTCCCTGTGGCAGCAGGCATGGAGAGT CAGGGCTGCCTTCATGGCAGTAGGCTCTAAGTGGGTGACTGGCCACAGGCCGAGAAAAGGGTACAGCCTCTAGGT TTGCATACATGCCTGGCATCTGTCTCCCCTTGTTCCTGAGTGGCCCCACATGGGGCTCTGAGCAGGCTGTATCTG

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><subunit 1 of 1, 412 aa, 1 stop

><MW: 46658, pI: 6.65, NX(S/T): 4

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EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEEMYQ
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI
PVIGPLKIREQQRSAVSTSWLLPYNYTWSPEKVFVQTPTINYTLRDYRKFFQDIGFEDGWLM
RQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLLGP

Important features:

Signal peptide:

amino acids 1-28

Potential lipid substrate binding site:

amino acids 147-164

N-glycosylation sites.

amino acids 99-102, 273-276, 289-292 and 398-401

Lipases, serine proteins

amino acids 189-201

Beta-transducin family Trp-Asp repeat

amino acids 353-365

GCCTACGGCGCGCCAAGGCGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCA GGTGGTGGCGCGCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTG AGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGAT GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGT GGTCGACGCGTATTTCCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAAC CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCAT CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAA CGCGGAGACCACCGAGGGCTACCAGCCGCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAA GGGGGACAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCA GCCCCTCTCTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGA CCTCAGCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT CAGCTTCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCA CTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCCACCCCTGTGCCGGT GGCCTCTGGGCTGCCTCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTG $\mathtt{CTCCCACCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTC}$ TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTC TGTGCCGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACG GAATAAATGTTTTCTCATTCAAAG

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<subunit 1 of 1, 224 aa, 1 stop

<MW: 24810, pI: 4.75, NX(S/T): 1

MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCVFN RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWFVGFC FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

Important features:

Type II Transmembrane domain:

amino acids 1-45

Other transmembrane domains:

amino acids 74-90, 108-126 and 145-161

N-glycosylation site.

amino acids 97-100

GAGCCACCTACCCTGCTCCGAGGCCAGGCCTGCAGGGCCTCATCGGCCAGAGGGTGATCAGTGAGCAGAAGGATG CCCGTGGCCGAGGCCCCCAGGTGGCTGGCGGGCAGGGGGACGGAGGTGATGGCGAGGAGCCGAGCCAGAGGGG GCCCTGCTCGTGCTTCGGCGGGGGTGCTACTCTGGTATTTCCTAGGGTACAAGGCGGAGGTGATGGTCAGC TTCCGCAGTGAAACCGCCAAAGCCCAGAAGATGCTCAAGGAGCTCATCACCAGCACCCGCCTGGGAACTTACTAC AACTCCAGCTCCGTCTATTCCTTTGGGGAGGGACCCCTCACCTGCTTCTTCTGGTTCATTCTCCAAATCCCCGAG CACCGCCGGCTGATGCTGAGCCCCGAGGTGGTGCAGGCACTGCTGGTGGAGGAGCTGCTGTCCACAGTCAACAGC TCGGCTGCCGTCCCCTACAGGGCCGAGTACGAAGTGGACCCCGAGGGCCTAGTGATCCTGGAAGCCAGTGTGAAA GACATAGCTGCATTGAATTCCACGCTGGGTTGTTACCGCTACAGCTACGTGGGCCAGGGCCAGGTCCTCCGGCTG ${\tt AAGGGGCCTGACCACCTGGCCTCCAGCTGCCTGTGGCACCTGCAGGGCCCCAAGGACCTCATGCTCAAACTCCGG}$ $\tt CTGGAGTGGACGCTGGCAGAGTGCCGGGACCGACTGGCCATGTATGACGTGGCCGGGCCCCTGGAGAAGAGGGCTC$ ATCACCTCGGTGTACGGCTGCAGCCGCCAGGAGCCCGTGGTGGAGGTTCTGGCGTCGGGGGCCATCATGGCGGTC GTCTGGAAGAAGGGCCTGCACAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGGTGGTCTTCCAGGCCTGT GAAGTGAACCTGACGCTGGACAACAGGCTCGACTCCCAGGGCGTCCTCAGCACCCCGTACTTCCCCAGCTACTAC TCGCCCCAAACCCACTGCTCCTGGCACCTCACGGTGCCCTCTCTGGACTACGGCTTGGCCCTCTGGTTTGATGCC TATGCACTGAGGAGGCAGAAGTATGATTTGCCGTGCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGT GGCTTGCGCATCCTGCAGCCCTACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACC TCCCAGATCTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTACAACCAGTCGGACCCCTGCCCTGGA GAGAGAAACTGCGTTTGCAGAGCCACATTCCAGTGCAAAGAGGACAGCACATGCATCTCACTGCCCAAGGTCTGT GATGGGCAGCCTGATTGTCTCAACGGCAGCGATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTCACC TTCCAGTGTGAGGACCGGAGCTGCGTGAAGAAGCCCAACCCGCAGTGTGATGGGCGGCCCGACTGCAGGGACGGC TCGGATGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGTCCTCCGAG ${\tt GGTGAGTGGCCATGGCAGCCTCCAGGTTCGGGGTCGACACATCTGTGGGGGGGCCCTCATCGCTGACCGC}$ TGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCATGGCCTCCACGGTGCTGTGGACCGTGTTCCTGGGC AAGGTGTGGCAGAACTCGCGCTGGCCTGGAGAGGTGTCCTTCAAGGTGAGCCGCCTGCTCCTGCACCCGTACCAC GAAGAGGACAGCCATGACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCGCTCGGCCGCCGTGCGC $\tt CCCGTCTGCCTGCCCGCGCGCTCCCACTTCTTCGAGCCCGGCCTGCACTGCTGGATTACGGGCTGGGGCGCCTTG$ GCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGCCGGCTACCGCAAGGGCCAAGAAGGATGCCTGTCAGGGT GACTCAGGTGGTCCGCTGGTGCAAGGCACTCAGTGGCCGCTGGTTCCTGGCGGGGCTGGTCAGCTGGGGCCTG GGCTGTGGCCGGCCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGTG $\tt GGGACAAGTATTCTGGCGGGGGGTGGGGGAGAGAGGCCCTGTGGTGGCAGGAGGTGGCATCTTGTCTCGTCC$ CTGATGTCTGCTCCAGTGATGGCAGGAGGATGGAGAAGTGCCAGCAGCTGGGGGTCAAGACGTCCCCTGAGGACC GCAGTGGCTCAGCAGCAAGAATGCTGGTTCTACATCCCGAGGAGTGTCTGAGGTGCGCCCCACTCTGTACAGAGG CTGTTTGGGCAGCCTTGCCTCCAGAGAGCAGATTCCAGCTTCGGAAGCCCCTGGTCTAACTTGGGATCTGGGAAT GGAAGGTGCTCCCATCGGAGGGGACCCTCAGAGCCCTGGAGACTGCCAGGTGGGCCTGCTGCCACTGTAAGCCAA

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><subunit 1 of 1, 802 aa, 1 stop

><MW: 88846, pI: 6.41, NX(S/T): 7

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YYNSSSVYSFGEGPLTCFFWFILQIPEHRRLMLSPEVVQALLVEELLSTVNSSAAVPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGQVLRLKGPDHLASSCLWHLQGPKDLML
KLRLEWTLAECRDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY
YDPFVLSVQPVVFQACEVNLTLDNRLDSQGVLSTPYFPSYYSPQTHCSWHLTVPSLDYGLAL
WFDAYALRRQKYDLPCTQGQWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP
GVRVHYGLYNQSDPCPGEFLCSVNGLCVPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS
LPKVCDGQPDCLNGSDEEQCQEGVPCGTFTFQCEDRSCVKKPNPQCDGRPDCRDGSDEEHCD
CGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIADRWVITAAHCFQEDSMASTVL
WTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPA
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG
KKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIQQVVT

Important features:

Type II transmembrane domain:

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447 and 509-512

Kringle domains.

amino acids 746-758 and 592-609

Homologous region to Kallikrein Light Chain:

amino acids 568-779

Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT $\tt CTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTACAACCAGTCGGACCCCTGCC$ TGCCCCAACGCCTGGATGAGAGAACTGCGTTTGCAGAGCCACATTCCAGTGCAAAGAGGA CAGCACATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTCACCTTCCAGTGTGAGGACCGG AGCTGCGTGAAGAAGCCCAACCCGCAGTGTGATGGGCGGCCCGACTGCAGGGACGGCTCGGA TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCTCCAGCCGCATTGTTGGTGGAGCTGTGT CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCGGGGTCGACACATCTGTGGG GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT GGCCTCCACGGTGCTGTGGACCGTGTTCCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG GAGAGGTGTCCTTCAAGGTGAGCCGCCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT GACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCGCTCGGCCGCCGTGCGCCC CGTCTGCCTGCCCGCGCTCCCACTTCTTCGAGCCCGGCCTGCACTGCTGGATTACGGGCT GGGGCGCCTTGCGCGAGGGCGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG ATCCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGCC CGGCTACCGCAAGGCCAAGAAGGATGCCTGTCAGGGTGACTCAGGTGGTCCGCTGGTGTGCA AGGCACTCAGTGGCCGCTGGTTCCTGGCGGGGCTGGTCAGCTGGGGCCTGGGCTGTGGCCGG CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT GACCTGAGGAACTGCCCCCCTGCAAAGCAGGGCCCACCTCCTGGACTCAGAGAGCCCAGGGC AACTGCCAAGCAGGGGGACAAGTAT

GGACGAGGCCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG CTCCGTGCCGCAAGTTTTCATTTTCCACCTTCTCTGCCTCCAGTCCCCCAGCCCCTGGCCG ACTTCTGTTTCTTGGGAGGGGTGTGGCGGGGCAGGATGAGCAACTCCGTTCCTCTGCTCTG TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG TTTAACCTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTCGGCCACAG CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAACCTTTTTCATCATTCACGGAT GGACGATGAGCGGTATCTTTGAAAACTGGCTGCACAAACTCGTGTCAGCCCTGCACACAAGA GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCTGGCCCACCAGCTTTACACGGA AGAAGGACGATTTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGGATCCTGC CGGGCCCATGTTTGAAGGGGCCGACATCCACAAGAGGCTCTCTCCGGACGATGCAGATTTTG TGGATGTCCTCCACACCTACACGCGTTCCTTCGGCTTGAGCATTGGTATTCAGATGCCTGTG TCCACCTCTTTGTTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTGCCTTCCAGTGCACT GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCAT TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGG CAGGCATGCCTTTCAGAGGTAACCTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA CCTCCTTCTTAATACCATGCTGCAGAGCAGGGCACATCCTAGCCCAGGAGAAGTGGCCAGCA CAATCCAATCAAATCGTTGCAAATCAGATTACACTGTGCATGTCCTAGGAAAGGGAATCTTT AAAAAAAAAAAAAAAAAA

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><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

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PLAHQLYTDAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV
GRITGLDPAGPMFEGADIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSLVNQDKPSFAFQCTDSNRFKKGICLS
CRKNRCNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

Important features:

Signal peptide:

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

CGGACGCGTGGGCGGACGCGTGGGCCTGGGCAAGGGCCGGGCCGGGCCGAGCCACCTCTTCCCCTCCCCGC CGGCAAAGTTTGGCCCGAAGAGGGAAGTGGTCTCAAACCCCGGCAGGTGGCGACCAGGCCAGACCAGGGGCGCTCG CTGCCTGCGGGCGGCTGTAGGCGAGGCGCCCCAGTGCCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAG AGAAGAGTGCGGCGGCGGACGAAAACAACTCCAAAGTTGGCGAAAGGCACCGCCCCTACTCCCGGGCTGCCG CCGCCTCCCCGCCCCAGCCTGGCATCCAGAGTACGGGTCGAGCCCGGGCCATGGAGCCCCCTGGGGAGGCGG CACCAGGAGCCTGGGCGCCGGGGCTCCGCCGACCCCATCGGGTAGACCACAGAAGCTCCGGGACCCTTCCG GCACCTCTGGACAGCCCAGGATGCTGTTGGCCACCCTCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAG ACCGGATTATTTTCCAAATCATGCTTGTGAGGACCCCCCAGCAGTGCTCTTAGAAGTGCAGGGCACCTTACAGA GGCCCCTGGTCCGGGACAGCCGCACCTCCCCTGCCAACTGCACCTGGCTCATCCTGGGCAGCAAGGAACAGACTG TCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCCTACGCTCCCCTCTCCAGCCAC TGATCTCCCTGTGTGAGGCACCTCCCAGCCCTCTGCAGCTGCCCGGGGGGCAACGTCACCATCACTTACAGCTATG CTGGGGCCAGAGCACCCATGGGCCAGGGCTTCCTGCTCTCCTACAGCCAAGATTGGCTGATGTGCCTGCAGGAAG AGTTTCAGTGCCTGAACCACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCTGTGGCGATGGCT TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCTGGATATACACACCTAGCCTCAGTCTCCCACCCCAGT CCTGCCATTGGCTGCTGGACCCCCATGATGGCCGGCGGCTGCCCTTCACAGCCCTGGACTTGGGCTTTG GAGATGCAGTGCATGTATGACGGCCCTGGGCCCCTGAGAGCTCCCGACTACTGCGTAGTCTCACCCACTTCA GCAATGCCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTTGTGTCCTACCACACAGTTGCTTGGAGCA GTGCTGACGGCACAGATGAGGAGGACTGCCCAGGCTGCCCACCTGGACACTTCCCCTGTGGGGCTGCTGGCACCT CTGGTGCCACAGCCTGCTGCCTGCTGACCGCTGCAACTACCAGACTTTCTGTGCTGATGGAGCAGATGAGA ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCCGCAAGGTCATTACAG TTCGCACCCAGGAGTACAGCATCTTTGCCCCCCTCTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGCACCCC CTTCCTACGGGCAGCTCATTGCCCAGGGTGCCATCCCACCTGTAGAAGACTTTCCTACAGAGAATCCTAATGATA ACTCAGTGCTGGGCAACCTGCGTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCCAGGTG AGGCTCCCCTCCCATCTGCTAGCACGTCTCCAGCCCCCACTACTGTCCCTGAAGCCCCAGGGCCCACTGCCCTCAC TGCCCCTAGAGCCATCACTATTGTCTGGAGTGGTGCAGGCCCTGCGAGGCCGCCTGTTGCCCAGCCTGGGGCCCC CAGGACCAACCCGGAGCCCCCTGGACCCCACACAGCAGTCCTGGCCCTGGAAGATGAGGACGATGTGCTACTGG TGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACC<u>TGA</u>GGGGACCTGGGGG CTCTACTGAGGCCTCTCCCCTGGGGGCTCTACTCATAGTGGCACAACCTTTTAGAGGTGGGTCAGCCTCCCCTCC ACCACTTCCTTCCCTGTCCCTGGATTTCAGGGACTTGGTGGGCCTCCCGTTGACCCTATGTAGCTGCTATAAAGT TAAGTGTCCCTCAGGCAGGGAGAGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCCAGTCCCT TCACCACCACCTGCTCCCCACGCCACCATTTGGGTGGCTGTTTTTAAAAAGTAAAGTTCTTAGAGGATCATA GGTCTGGACACTCCATCCTTGCCAAACCTCTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAACTAGAGA CCCTCCAGCCCCAAGGGGAGGATTTGGGCAGAACCTGAGGTTTTGCCATCCACAATCCCTCCTACAGGGCCTGG CTCACAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAA **GGAATCATACATCTC**

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<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

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Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

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><subunit 1 of 1, 152 aa, 1 stop

><MW: 17170, pI: 9.62, NX(S/T): 1

MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTFFIIAQAPEPYIVITGFEVTVILFFILL YVLRLDRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTLTVGGGVFALVTAVCCLAD GALIYRKLLFNPSGPYQKKPVHEKKEVL

Important features:

Potential type II transmembrane domain:

amino acids 26-42

Other potential transmembrane domain:

amino acids 44-65, 81-101 and 109-129

Leucine zipper pattern

amino acids 78-99 and 85-106

N-myristoylation site.

amino acids 110-115

Ribonucleotide reductase large subunit protein

amino acids 116-127

GGGCGAGAAGTAGGGGAGGGCGTGTTCCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTGTAAAAGGCCACGTG
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTTATNATCGCACAAGCCCC
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATACTTTTAT
ATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTTGGCCTTTGATATTATCAAC
TCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTTTGGCACTGATACCAGAAACCAC
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTNTTGCCGAC

CAGCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG CTGGGCGCCCCCGGGCCCCGCCGTGGGCATGGCCACTGGCCCGGGCGCTGCTGC CTCTGCTGGCCCAGTGGCTCCTGCGCGCCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTG CCCCTCCGGGTGGCCGCGCCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCC TGCCGAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC CTGGAGATGCTGATCGGGACCCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG TAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAA CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTTGCCTGGGATTAAATGGAATGGAATAC TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC ${\tt CTGGTGACAGCAAGCATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC}$ ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTG AAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC CATCGTGGACAGTGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGG AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG CTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCT GAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTCAGC CCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCATCCACAAAT GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAA GAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT CCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG CCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTT AATCGTCCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCCGTGACCCTGAGGTCGTCA ATGATGAGTCCTCTGGTCAGACATCGCTGGAAA**TGA**ATAGCCAGGCCTGACCTCAAGCAA CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCCGGGGATCGATGGTGGCG $\mathtt{CTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGATTCAC$ TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA AAAAAAACTTCATTCTAA

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><subunit 1 of 1, 518 aa, 1 stop

><MW: 56180, pI: 5.08, NX(S/T): 2

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Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

CGCCTCCGCCTTCGGAGGCTGACGCCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG GCAGCCGCCTGGCGGCGATCCAGGGCGGTGCGGGGCCTGGGCGGGGGCCGGGGCGCGCC GGCATGGAGGCGCTGCTGCTGGGCGCGGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA CAACCTGGTGAAGGCCCCGCCGTGCGGCGGCATGGGCAACCTGCGGGGCCGCACGGCCGTGG TCACGGGCGCCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG GGAGAGTGGGAACAATGAGGTCATCTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC GGTATCAGTTCCTGTGGCCGGACCCGTGAGGCGTTTAACCTGCTGCTTCGGGTGAACCATAT TGGTGGTGGTAGCCTCAGCTGCCCACTGTCGGGGACGTCTTGACTTCAAACGCCTGGACCGC CCAGTGGTGGGCTGCGGCAGGAGCTGCGGCCATATGCTGACACTAAGCTGGCTAATGTACT GTTTGCCCGGGAGCTCGCCAACCAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCCACC CAGGGCCTGTGAACTCGGAGCTGTTCCTGCGCCATGTTCCTGGATGGCTGCGCCCACTTTTG CGCCCATTGGCTTGGTGCTCCGGGCACCAAGAGGGGGTGCCCAGACACCCCTGTATTG TGCTCTACAAGAGGGCATCGAGCCCCTCAGTGGGAGATATTTTGCCAACTGCCATGTGGAAG AGGTGCCTCCAGCTGCCCGAGACGACCGGCCAGCCATCGGCTATGGGAGGCCAGCAAGAGG CTGGCAGGGCTTGGGCCTGGGGAGGATGCTGAACCCGATGAAGACCCCCAGTCTGAGGACTC AGAGGCCCCATCTTCTCTAAGCACCCCCCCCCTGAGGAGCCCACAGTTTCTCAACCTTACC CCAGCCCTCAGAGCTCACCAGATTTGTCTAAGATGACGCACCGAATTCAGGCTAAAGTTGAG CCTGAGATCCAGCTCTCCTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCTT GAAAACCTCGGATGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCCTGGTTGAAGGAAT AATGGGTGATTATTTCTTCCTGAGAGTGACAGTAACCCCAGATGGAGAGATAGGGGTATGCT AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTCAGGCCCCACCCTTATTGATTCTG ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG TGAACTGATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCCATGTTAATGAAGCG GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGGGGCCTG GGATCTGAACCCAAGGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA GTCAGGGCAGGCAGCTGGTATCGAGGTGCCCCATGGGAGTAAGGGGACGCCTTCCGGGCGG ATGCAGGGCTGGGGTCATCTGTATCTGAAGCCCCTCGGAATAAAGCGCGTTGACCGCCAAAA AAAAAAAAAAAAA

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<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGRTAVVTGANSGIGKMTALELARRGAR
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG
ISSCGRTREAFNLLLRVNHIGPFLLTHLLLPCLKACAPSRVVVVASAAHCRGRLDFKRLDRP
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHPGPVNSELFLRHVPGWLRPLLR
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDDRAAHRLWEASKRL
AGLGPGEDAEPDEDPQSEDSEAPSSLSTPHPEEPTVSQPYPSPQSSPDLSKMTHRIQAKVEP
EIQLS

Important features:

Signal peptide:

amino acids 1-16

Glycosaminoglycan attachment site.

amino acids 46-49

Short-chain alcohol dehydrogenase family

amino acids 37-49 and 114-124

GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTCCTGCTCATCATGGGAGGCATGGCTCAG GACTCCCCGCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGC GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGCGCT TTTACTCTGGAATGTGGGCCGCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTG GCCCTCCAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGGG CAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAAAATGTGACACTGCTGAACCCGGAT CCTGCAGAGGGCCCCAAGCCTAGACCGGCGGTGTGGCTCAGCTGGAAGGTCAGTGGCCCTGCTGCCCCAA TCTTACACGGCCTTGTTCAGGACCCAGACTGCCCCGGGAGGCCAGGGGAGCTCCGTGGGCAGAGGAGCTGCTGGCC GGCTGGCAGAGCGCAGAGCTTGGAGGCCTCCACTGGGGCCAAGACTACGAGTTCAAAGTGAGACCATCCTCTGGC CGGGCTCGAGGCCCTGACAGCAACGTGCTGCTCCTGAGGCTGCCGGAAAAAGTGCCCAGTGCCCACCTCAGGAA GTGACTCTAAAGCCTGGCAATGGCACTGTCTTTGTGAGCTGGGTCCCACCACCTGCTGAAAACCACAATGGCATC ATCCGTGGCTACCAGGTCTGGAGCCTGGGCAACACATCACTGCCACCAGCCAACTGGACTGTAGTTGGTGAGCAG GGTCCCTGGACCCTGGAGCAGCTGAGGGCTACCTTGAAGCGGCCTGAGGTCATTGCCACCTGCGGTGTTGCACTC $\tt TGGCTGCTGCTTCTGGGCACCGCCGTGTGTATCCACCGCCGGCGCGCGGGCTAGGGTGCACCTGGGCCCAGGTCTG$ GACCCACTAGACTGTCGTCGCTCCTTGCTCTCCTGGGACTCCCGAAGCCCCGGCGTGCCCCTGCTTCCAGACACC GGACTCTCTCCCCGCTTGTCTCTGGCCCCTGCAGAGGCTTGGAAGGCCCAAAAAGAAGCAGGAGCTGCAGCAT GCCAACAGTTCCCCACTGCTCCGGGGCAGCCACTCCTTGGAGCTCCGGGCCTGTGAGTTAGGAAATAGAGGTTCC AAGAACCTTTCCCAAAGCCCAGGAGCTGTGCCCCAAGCTCTGGTTGCCTGGCGGGCCCTGGGACCGAAACTCCTC AGCTCCTCAAATGAGCTGGTTACTCGTCATCTCCCTCCAGCACCCCTCTTTCCTCATGAAACTCCCCCAACTCAG $\tt CTTAGCCCCTGCAGTCCCCCTAGCCCCCAGGCCTCTTCCCTCTCTGGCCCCAGCCCAGCCTTCCAGTCGCCTGTCC$ AGCTCCTCACTGTCATCCCTGGGGGAGGATCAAGACAGCGTGCTGACCCCTGAGGAGGTAGCCCTGTGCTTGGAA $\tt CTCAGTGAGGGTGAGGAGACTCCCAGGAACAGCGTCTCTCCCATGCCAAGGGCTCCTTCACCCCCCACCACTAT$ GGGTACATCAGCGTCCCAACAGCCTCAGAGTTCACGGACATGGGCAGGACTGGAGGAGGGGGTGGGGCCCAAGGGG GGAGTCTTGCTGTGCCCACCTCGGCCCTGCCTCACCCCCACCCCAGCGAGGGCTCCTTAGCCAATGGTTGGGGC GCTCACTTTGCCCGGGCCCTGGCAGTGGCTGTGGATAGCTTTGGTTTCGGTCTAGAGCCCAGGGAGGCAGACTGC GTCTTCATAGATGCCTCATCACCTCCCTCCCCACGGGATGAGATCTTCCTGACCCCCAACCTCTCCCTGCCCCTG TGGGAGTGGAGGCCAGACTGGTTGGAAGACATGGAGGTCAGCCACACCCAGCGGCTGGGAAGGGGGATGCCTCCC TGGCCCCTGACTCTCAGATCTCTTCCCAGAGAAGTCAGCTCCACTGTCGTATGCCCAAGGCTGGTGCTTCTCCT ACCTGGGCTGTGTGTGGGCTCTTGGCCTGTGTTTCTCTGCAGCTGGGGTCCACCTTCCCAAGCCTCCAGAGAG TTCTCCCTCCACGATTGTGAAAACAAATGAAAACAAAATTAGAGCAAAGCTGACCTGGAGCCCTCAGGGAGCAAA $\tt CTGAGGAGCAGCCTGCTGCTGCTCTCCCCCACCATTTGGATCACAGGAAGTGGAGGAGCCAGAGGTGCCTTT$ TATGAGACCGTAGGTCAAAAGCACCATCCTCGTACTGTTGTCACTATGAGCTTAAGAAATTTGATACCATAAAAT GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404</pre>

<subunit 1 of 1, 985 aa, 1 stop</pre>

<MW: 105336, pI: 6.55, NX(S/T): 7

MGGMAQDSPPQILVHPQDQLFQGPGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHHLLP DGTLLLLOPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM VAVVGEOFTLECGPPWGHPEPTVSWWKDGKPLALOPGRHTVSGGSLLMARAEKSDEGTYMCV ATNSAGHRESRAARVSIOEPODYTEPVELLAVRIOLENVTLLNPDPAEGPKPRPAVWLSWKV SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG ${\tt PDSNVLLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP}$ ANWTVVGEOTOLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGPW TLEOLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD HSDSOWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTST FYGSLIAELPSSTPARPSPQVPAVRRLPPQLAQLSSPCSSSDSLCSRRGLSSPRLSLAPAEA WKAKKKOELOHANSSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS SSNELVTRHLPPAPLFPHETPPTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPPSPQASS LSGPSPASSRLSSSSLSSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY GYISVPTASEFTDMGRTGGGVGPKGGVLLCPPRPCLTPTPSEGSLANGWGSASEDNAASARA SLVSSSDGSFLADAHFARALAVAVDSFGFGLEPREADCVFIDASSPPSPRDEIFLTPNLSLP LWEWRPDWLEDMEVSHTQRLGRGMPPWPPDSQISSQRSQLHCRMPKAGASPVDYS

Important features:

Transmembrane domain:

amino acids 448-467

N-glycosylation sites:

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

N-myristoylation sites.

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

Phosphotyrosine interaction domain proteins

amino acids 740-753

 $\verb|CCCAGGTTATGAAGCCCTGGAGGGCCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT| \\$ CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT GGGATCCTCTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGACCAGGAGACAAT GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGA ACCTCACCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG TCTTTACTGATCTCTGTTCGTCTTTCCAGGACCCTGCTGTCCTCCCCTCCCCTTCTCCCAC CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCC CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG GCTGAGGCCCCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCATGCAGC TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCCTGGTGCTGAGCCTTCTGTCAGC CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGÀAGCC CCTTCCCAGGCCCCTGAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGA GCTGGGCTTCTCGAAGTTTGTCTCAGCG**TAG**GGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAG TCCAGCTGCCCGGACTCCAGGCTCTCCCCACCCTCCCAGGCTCTCCTCTTGCATGTTCCA GCCTGACCTAGAAGCGTTTGTCAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG GAGACTGGGACATCCCTGATAGGTTCACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACTCCTGGGC TGGCGTCCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCT GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT GTGAAAAACGTGATTCCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG GACTCTGAATTCTAACAATGCCCAGTGACTGTCGCACTTGAGTTTGAGGGCCAGTGGGCCTG ATGAACGCTCACACCCCTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCC CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCCTGAGGCCTGCTAAG TCCAGGCCTTGGTCAGGTCAGGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCCTTTTGGAAAAAATGATGAAGA AAACCTTGGCTCCTTGTCTGGAAAGGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA GAAAAGTAGAAAACCAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTCGGGGGTGGTGGTAAAGTA GCACAACTACTATTTTTTTTTTTTCCATTATTATTGTTTTTTAAGACAGAATCTCGTGCT GCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACTCCGCCTCCTGGGTTCAAGTGATT CTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG TCTGGCCCTATTTCCTTTAAAAAGTGAAATTAAGAGTTGTTCAGTATGCAAAACTTGGAAAG ATGGAGGAGAAAAGGAAAAGGAAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT TATTTCGTTTTGTTGTACTTCCTTCCACTCTTTTCTTCACATAATTTGCCGGTGTTCTT TTTACAGAGCAATTATCTTGTATACAACTTTGTATCCTGCCTTTTCCACCTTATCGTTCC GCTGCATAAAAAAAAAAAAA

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196</pre>

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

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Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGGGTGCAGCTGCAGGCGTGGGGGTGGCAGGA GCCGCAGAGCCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC GCTCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA GCCCTGTTTCTCCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCATCCCAA AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAG TCAGCTGCCTGCTACCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC TTATTTCACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCCGAACGTCCCCAAC GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTTACTGGGAGGCCTGGAGGCATCACTGCC AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTC**TAG**GATGGACGGAACCATGCA CAGCAGGCTGGGAAATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA AAGGATGGTTGAACGTGAAA

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187
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YEADGSTNNGIFQINSRRWCSNLTPNVPNVCRMYCSDLLNPNLKDTVICAMKITQEPQGLGY
WEAWRHHCQGKDLTEWVDGCDF</pre>

Important features:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homolgous region to Alpha-lactalbumin / lysozyme C proteins. amino acids 34-58 (catalytic domain), 111-132 and 66-107

AGCCGCTGCCCCGGGCCGCGCGCGCGCGCACC<u>ATG</u>AGTCCCCGCTCGTGCCTGCGTTC GCTGCGCCTCCTCGTCTTCGCCGTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCA AGCTGTCGTCGGTGGGGAGCATCTCAGAGGAGAGACGTGCGAGAAACTCAAGGGCCTGATC CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCCGGAACCGGCGCTGGAACTGCTCCACAC TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTG TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGCAGCAGTGGGGAGCT GGAGAAGTGCGGCTGTGACAGGACAGTGCATGGGGTCAGCCCACAGGGCTTCCAGTGGTCAG GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCCGGCAG GAAGGCCATCCTGACACACATGCGGGTGGAATGCAAGTGCCACGGGGTGTCAGGCTCCTGTG AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTCACGCACTGAAGGAG AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACC ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG ACTTCTGTGAGCAGGACATGCGCAGCGGCGTGCTGGGCACGAGGGGCCCGCACATGCAACAAG GGTGGAGCTGGAACGCTGCAGCTGCAAATTCCACTGGTGCTGCTTCGTCAAGTGCCGGC AACCACCTAGTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCCACCACCTACCCCAAGA ACCAGGCAGCCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAAGCCTGGGCCTTTGTGGCT CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGCAGACCTAAGGTGGAGTAACAAGGAGTAT TACCACCACATGGCTACTGACCGTGTCATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATA GGTACCGACTTGATGGAAGTCACACCCTCTGGAAAAAAGAACTCTTAACTCTCCAGCACACA TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG GAACAAGCAGATACCAGGTCAAGGGCACCAGGTTCATTTCAGCCCTTACATGGACAGCTAGA GGTTCGATATCTGTGGGTCCTTCCAGGCAAGAAGAGGGGAGATGAGAGCAAGAGACGACTGAA GTCCCACCCTAGAACCCAGCCTGCCCCAGCCTGCCCCTGGGAAGAGGAAACTTAACCACTCC ${\tt CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT}$ GAGAGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCCGAGTCACCTTTCACAGCACTGTTCCTC

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328</pre>

<subunit 1 of 1, 351 aa, 1 stop</pre>

<MW: 39052, pI: 8.97, NX(S/T): 2

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VMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSAGVAFAV
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFVDVRERSKGASSSRALM
NLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRR
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC
CGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT CGCCATGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGC CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTC ACCACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC GGCGCTGCTTGACGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGCGCTGG GTGCCCTGAAGGAGGTCGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGAGAGCGCCCT GCGGGAACTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACG TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACTCCTGCGAGCCG TGCCCCACGTCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC GTGGGCGCGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC CAGCCACTGGAACCAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTCATGATGC TGCACACGGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG AAAAGGCACAACTGC**TGA**CCCCGCCCAGTGCCCTGGAGCCGCGCCCATTGCAGCATGTCGTA TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTCTTCCT CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACCTAACC TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAA CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACTGGA AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTTGAGAAAATGAAAAAA

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352</pre>

<subunit 1 of 1, 293 aa, 1 stop

<MW: 32562, pI: 6.53, NX(S/T): 2

MDTTRYSKWGGSSEEVPGGPWGRWVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA LLDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAELGEAQAKLMEQESALR ELRERVTQGLAEAGRGREDVRTELFRALEAVRLQNNSCEPCPTSWLSFEGSCYFFSVPKTTW AAAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS HWNQGEPNDAWGRENCVMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:

Type II transmembrane domain:

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

GCCAGGGGAAGAGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCG GCAGCCCCGCCGCCCCCGCAGCCCCTTCTCCTCCTTTCTCCCACGTCCTATCTGCCTCTCG CGCGCTCCCGCTGCTGCCGGGTG<u>ATG</u>GAAAACCCCAGCCCGGCCGCCCCTGGGCAAG CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA CGGCCTTCCCCAAGCAGTACCCCCTGTTCCGCCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTCAGTAACGGGCTGCG CGACTTTGCGGAGCGCGGGGGGCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGGAGG CGCTGCAGAGCGTGCACGAGGTGTTTTCGGCGCCCCGCCGTCCCCAGCGGCACCGGGCAGACG ${\tt TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCC}$ CAGCCCGACTGGTTCGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG ${ t TCCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCCTCTCTCCCAG$ CCACCGGCCAACTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGA AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTC CCTGTGGTCGTCCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA CTCGCTACGTCCGGGTCCAGCCCGCCAACAACGGGAGCCCCTGCCCCGAGCTCGAAGAAGAG GCTGAGTGCGTCCTGATAACTGCGTC<u>TAA</u>GACCAGAGCCCCGCAGCCCCTGGGGCCCCCCG GAGCCATGGGGTGTCGGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCACAGGG GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCCGACCATCTCTGCACTGAAGGGCCCT CCCCCGTGTCCCGTCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTC CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGTCCTTCATCG TCCAGGGGCCTGGCTCCCACGTGGTTGCAGATACCTCAGACCTGGTGCTCTAGGCTGTGCTG AGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTGAATAAATGGGGCGG TTTCGGAAGCGTCAGTGTTTCCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCT

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><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

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Important features:

Signal peptide:

amino acids 1-26

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGTCTTGCGTGA TATTGACAAACTGAAGCTTTCCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGA CAGCTTTAGTGGCCGGCCGGCCGCTCTCATCCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC CAAGATGAGCAACATCTACATCCAGGAGCCTCCCACGAATGGGAAGGTTTTATTGAAAACTA CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGCAGAAATTTT ATCCAACTTTGTTTGGAAGCTTATTATGACAATACCATTTTTCATAGAGTTGTGCCTGGTTT CATTCAAAGATGAATTTCATTCACGGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCA* AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACACTGGGTCGAGCAGATGAACT TAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAAGCTGT GAGGTTTTGTTTAATCCTTTTGATGACATCATTCCAAGGGAAATTAAAAAGGCTGAAAAAAGA GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTTAGTTTACTTT CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT TGTAGAAAGTGAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC AGTCAGCCGCAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAAAACGGGAACTCTTAGCAG GCCCCTCCAGATGGTGCTGTTGCCGAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTTGAG GAAGCAACAGTCAAAGAAGGGAACTTCCCGGGAAGATCAGACCCTTGCACTGCACCAGT TTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGAA GTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGT GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA GAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTTGTAACAGCCATTG TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTTGAACCTGTTGTCTGGTTTTG AAAAACAATTATCTTGTTTTGCAAATTGTGGAATGATGTAAGCAAATGCTTTTGGTTACTGG TACATGTGTTTTTTCCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCCT TCCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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><subunit 1 of 1, 472 aa, 1 stop

><MW: 53847, pI: 5.75, NX(S/T): 2

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VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFNPFDDIIPREIKRLKKEK
PEEEVKKLKPKGTKNFSLLSFGEEAEEEEEEVNRVSQSMKGKSKSSHDLLKDDPHLSSVPVV
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKSV
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEEAPPDGAVAEYRREKQKYEALRK
QQSKKGTSREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMSHVLQFEDKSRKVK
DASMQDSDTFEIYDPRNPVNKRRREESKKLMREKKERR

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature. amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

CCCGCCTCGGCTTTGAGGCGAGAGAGTGTCCCAGACCCATTTCGCCTTGCTGACGGCGTCG AGCCCTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC GTGGCCGCCGGCGGACCAGCACGCGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAA CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTG CTCCTTCAAGTGGTTTTGGAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA GGAGGAACAAATACAGGTGCCTTGCACACCAAGAGGCCTCAAGTGGTCACCAAATATGGAAC CCTGCAAGGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCCT TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAGCCCTGGAAA GGAATCAGAGATGCTÄCCACCTACCCGCCTGGATGGAGTCTCGCTCTGTCGCCAGGCTGGAG TGCAGTGGCACGATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGAGTCTCCTGC CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCCTGGGGCCAGCTGGCCTCG GAACGTGTACGCGCCGGCGCGCGCGCGCGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCC GAGAAAGTGGTGCTGGTGTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGA CGACAGCCACGCGCGGGAACTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGC AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTCGGCCAGTCGGCG GGGGCCATGAGCATCTCAGGACTGATGATGTCACCCCTAGCCTCGGGTCTCTTCCATCGGGC CATTTCCCAGAGTGGCACCGCGTTATTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGG CCAAGAAGGTTGCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCCTCCAACT GAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG TGATCCCAGATGACCCTTTGGTGCTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCTTATAATATCACCAAGGAGCAGGT ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA ACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACTGCTCAC TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCA**TGA**AGCTCAAGGAGAAGAAGATGGC TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC TATGCAGGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGACTAGCCA TGGACATACCTGGGGACAAGAGTTCTACCCACCCCAGTTTAGAACTGCAGGAGCTCCCTGCT GCCTCCAGGCCAAAGCTAGAGCTTTTGCCTGTTGTGTGGGACCTGCACTGCCCTTTCCAGCC TGACATCCCATGATGCCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC ACCACACTGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTTTCCCTTCTTCAAATCCT CCCACCCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGGTCGACCCAGACTGCCACTGC TCACATTGGCCTGGAGGCCTAGGGCAGGTTGTGACATGGAGCAAACTTTTGGTAGTTTGGGA TCTTCTCTCCCACCCACACTTATCTCCCCCAGGGCCACTCCAAAGTCTATACACAGGGGTGG TCTCTTCAATAAAGAAGTGTTGATTAGAAAAAAAAAAA

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<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

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Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT GCTGTCCTCGCTGCTGGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG AGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCCGA CAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC CAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGAGAGGTGGAAATGAGCACCCGGGGCC GATTCCAGCTCACTGGGGATCCCGCCAAGGGGAACTGCTCCTTGGTGATCAGAGACGCGCAG ATGCAGGATGAGTCACAGTACTTCTTTCGGGTGGAGAGGGAAGCTATGTGACATATAATTT CATGAACGATGGGTTCTTTCTAAAAGTAACAGTGCTCAGCTTCACGCCCAGACCCCAGGACC ACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC GTCCGACTCCGTGTGGCCTATGCCCCCAGAGACCTTGTTATCAGCATTTCACGTGACAACAC GCCAGCCCTGGAGCCCCAGCCCCAGGGAAATGTCCCATACCTGGAAGCCCAAAAAGGCCAGT TCCTGCGGCTCCTCTGTGCTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCCTGCAG AACAGAGTCCTCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGG GGTGAAGGCTGGGGATTCAGGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGC AGCGAGCCCTGGACCTCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAA GCAAACAGGACAGTCCTGGAAAACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCA GGGGACAGGTTCTGAGCCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTT CAAGTGGAGCACGAAGGAGTTCACCTGCCACGCTCGGCACCCACTGGGCTCCCAGCACGT CTCTCTCAGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAG CGTTTCTGGGAATCGGCATCACGGCTCTTCTTTTCCTCTGCCTGGCCCTGATCATCATGAAG ATTCTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACAGCAC GATCCTGGATTACATCAATGTGGTCCCGACGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA AAGAACCAGAAAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACTCAAGC CCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCA GACCCAGGCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTC CAA**TGA**GGGTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAAGGTAGAGTAAGAG CTCTCTTTCTCTCTCTTTTAAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCTGTAATC CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTCGGGAGTTCGAGACCAGCCTG GCCAACTTGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCAGG CGCCTGTAATCCTACCTACTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG AGGTTGCAGTGAGCCAAGATCACACCATTGCACGCCAGCCTGGGCAACAAAGCGAGACTCCA TCTCAAAAAAAATCCTCCAAATGGGTTGGGTGTCTGTAATCCCAGCACTTTGGGAGGCTA AGGTGGGTGGATTGCTTGAGCCCAGGAGTTCGAGACCAGCCTGGGCAACATGGTGAAACCCC ATCTCTACAAAAATACAAAACATAGCTGGGCTTGGTGGTGTGCCTGTAGTCCCAGCTGT CAGACATTTAAACCAGAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACC TACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAGGATGAGACAGGAGGTCCG ATCCCACCAAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCGTCCTCACTGCTACACTCCT GACAGCACCATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCA AAAGGGGGAGGAATGAATAATCCACCCCTTGTTTAGCAAATAAGCAAGAAATAACCATAAAA GTGGGCAACCAGCAGCTCTAGGCGCTGCTCTTGTCTATGGAGTAGCCATTCTTTTGTTCCTT TACTTTCTTAATAAACTTGCTTTCACCTTAAAAAAA

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><subunit 1 of 1, 544 aa, 1 stop

>< MW: 60268, pI: 9.53, NX(S/T): 3

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AVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGS
YVTYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPL
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSL
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHP
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPR
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEP
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

Important features:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

Immunoglobulins and major histocompatibility complex proteins signature.

amino acids 365-371

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCA**ATG**AACTGTTATTTACTGCTGCGTTT AAGTCAAGCAGCCAGTGCGATCTCATTTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA CAATGGAAACAATTCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA GTTTGTCATCAAAGTTTCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC ATATTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG TCTGGAACAACAAGTGTATTAATTAAACTTTCAGATGTTAATGACAATAAGCCTATATTTAA AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT GATTCGCAAACATTTGACATTATTACTAATCATGAAACTCAAGAAGGAATAGTTATATTAAA AAAGAAAGTGGATTTTGAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAACCATC ATGTTCCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCACTTTCATTAAGATCCAG GTGGAAGATGTTGATGAGCCTCCTCTTTTCCTCCTTCCATATTATGTATTTGAAGTTTTTGA AGAAACCCCACAGGGATCATTTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCAATATCAATGATAATGGTACAATC ACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC AGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAACATCA ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTTGTGAAAATGCAGGCTCT GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTT TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAAGTTTTACAATCATAGATAATCAAG ATAACACAGCTGTCATTTTGACTAATAGAACTGGTTTTAACCTTCAAGAAGAACCTGTCTTC TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTAC CATCCATGTCTGTGACTGTGGCAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTTGCATTATGATCATA TTTGGGTTTATTTTTTGACTTTGGGTTTAAAACAACGGAGAAAACAGATTCTATTTCCTGA GAAAAGTGAAGATTTCAGAGAGAATATATTCCAATATGATGATGAAGGGGGTGGAGAAGAAG ATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT CGGAAAACCACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA CAGTGCCATATTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG CCCCTCCTTTTGATTCCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCC CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAATAAT**TAG**G GCTTTTTACCATCAAAATTTTTAAAAGTGCTAATGTGTATTCGAACCCAATGGTAGTCTTAA AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC CTGGAGTAAATACTCCATGGTTATTTTAAGCTACCTACATGCTGTCATTGAACAGAGATGTG GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAAATAATG TAGGAAGATATTAAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT CATTATTTACTTAGGAAAGAGTAAAAATACCAAACGAGAAAATTTAAAGGAGCAAAAATTTG CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCCATGAAGTATTGTTTCCTTTAT TTAAA

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><subunit 1 of 1, 772 aa, 1 stop

><MW: 87002, pI: 4.64, NX(S/T): 8

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GRAVEPESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARL
LYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSD
VNDNKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
TQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL
PYYVFEVFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR
DESIEEHHFYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP
SLTSTNTLTIHVCDCGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESAVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518, 516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

ATTTCAAGGCCAGCCATATTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTNTA
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAAACTTTCAGATGTTAATGACAA
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC
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CCAGAGCTTCTCCAGCGGCGCGCGCGAGCGGGCTCCCCGCCTTAACTTCCTCCGCGGGG CCCAGCCACCTTCGGGAGTCCGGGTTGCCCACCTGCAAACTCTCCGCCTTCTGCACCTGCCA CCCCTGAGCCAGCGCGGGCCCCGAGCGAGTCATGCCCAACGCGGGGCTGCAGCTGTTGGGC TTCATTCTCGCCTTCCTGGGATGGATCGCCCATCGTCAGCACTGCCCTGCCCCAGTGGAG GATTTACTCCTATGCCGGCGACAACATCGTGACCGCCCAGGCCATGTACGAGGGGCTGTGGA TGTCCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAAT CTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGAT AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGC AGAAGATGAGGATGGCTGTCATTGGGGGTGCGATATTTCTTCTTGCAGGTCTGGCTATTTTA GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCCCAGT TTCTGGGAGGTGCCCTACTTTGCTGTTCCTGTCCCGAAAAACAACCTCTTACCCAACACCA AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAAGACTACGTGTGACACAGAGGCAAAAG GAGAAAATCATGTTGAAACAAACCGAAAATGGACATTGAGATACTATCATTAACATTAGGAC ACCCATGTGTTAAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTTCCTCA ATATAGGAGGGAAGATTTTTCCATTTGTATTACTGCTTCCCATTGAGTAATCATACTCAAAT ATAGACAGTAAAATACTATTCTCATTATGTTGATACTAGCATACTTAAAATATCTCTAAAAT AGGTAAATGTATTTAATTCCATATTGATGAAGATGTTTATTGGTATATTTTCTTTTTCGTCC TTATATACATATGTAACAGTCAAATATCATTTACTCTTCTTCATTAGCTTTGGGTGCCTTTG CCACAAGACCTAGCCTAATTTACCAAGGATGAATTCTTTCAATTCTTCATGCGTGCCCTTTT CATATACTTATTTTATTTTTTACCATAATCTTATAGCACTTGCATCGTTATTAAGCCCTTAT TTGTTTTGTGTTTCATTGGTCTCTATCTCCTGAATCTAACACATTTCATAGCCTACATTTTA GTTTCTAAAGCCAAGAAGTTTATTACAAATCAGAACTTTGGAGGCAAATCTTTCTGCATG ACCAAAGTGATAAATTCCTGTTGACCTTCCCACACAATCCCTGTACTCTGACCCATAGCACT CTTGTTTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTTGT AACACAACTTTATTGATTGAATTTTTAAGCTACTTATTCATAGTTTTATATCCCCCCTAAACT ACCTTTTTGTTCCCCATTCCTTAATTGTATTGTTTTCCCAAGTGTAATTATCATGCGTTTTA TATCTTCCTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA ATCTGGTGACAAATATTCTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTTCTACCTCTTTT TTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAGAAGAGGTAGTGTGAATATTAA TTAGTTTATATTACTCTTATTCTTTGAACATGAACTATGCCTATGTAGTGTCTTTATTTGCT CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACGTACCTTCATGTGATT CACTGCCTTCCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACACACATACCTTCAT GTGGTTCAGTGCCTTCCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACGCACATAC CTTCATGTGGCTCAGTGCCTTCCTCTCTACCAGTCTATTTCCATTCTTTCAGCTGTGTCT GACATGTTTGTGCTCTGTTCCATTTTAACAACTGCTCTTACTTTTCCAGTCTGTACAGAATG CTATTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTTGGCACTGGTGTCTGGAGACCTG GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGAGCAAGGCATTTGGCTGCTGTAA GCTTATTGCTTCATCTGTAAGCGGTGGTTTGTAATTCCTGATCTTCCCACCTCACAGTGATG TTGTGGGGATCCAGTGAGATAGAATACATGTAAGTGTGGTTTTGTAATTTAAAAAGTGCTAT ACTAAGGGAAAGAATTGAGGAATTAACTGCATACGTTTTTGGTGTTTTCAAATGTTTGA AAATAAAAAAAATGTTAAG

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><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

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Important features:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein amino acids 119-133

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 ${\tt TCATAGGGGGGCGCGATATTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA} \\ {\tt TGGCAATAGAATCGTTCAAGAATTNTATGACCCTATGACCCCAGTCAATGCCAGGTACGAAT} \\ {\tt TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA} \\ {\tt CTTTGCTGTTCCTG} \\$

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<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

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Important features:

Transmembrane domain:

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT

AAATGACACCNTTCCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCCCCAGCATGCTG

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CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTTTGA

CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT

AAATTGTATTGGTTCATGTAGTGAAGTCAAACTGTTATTCAGAGATGTTTAATGCATATTTA

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GCGAGCTCCGGGTGCTGTGGCCGGCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGAGA GGCTCCCAGCTGCAGCGTCCCCGCCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC CTCGGGGACCAAACAAGCCTGGCAGGGTCTCACTTTGTTGCCCAGGCTGGAGTTCAGTGCCA TGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAAGCGATCCTGCTGAGTAGCTGGGA CTACAGGACAAATTAGAAGATCAAA**ATG**GAAAATATGCTGCTTTGGTTGATATTTTTCACC GGTACCCCGGATTGTCAGTGAAAGGACTTTCCATCTCACCAGCCCCGCATTTGAGGCAGATG CTTTCTGAATTGGAGGATTATCTTTCCTATGAGACTGTCTTTGAGAATGGCACCCGAACCTT AACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG TATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTCAGCATCTTGGACAAA AGGTTCTTAACCAATTTCCCTTTCAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT TCTCATTTCCCCTCAGCATGTTCTAACTGCTGCCCACTGTGTTCATGATGGAAAGGACTATG TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG AAACGTCGAGGTTCTAAGAGGAGCAGGAGAGAGCTAGTGGTGGTGACCAAAGAGAGGGTAC CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAAAAATCTGGCCGGGGTC AGAGGATTGCCGAAGGGAGGCCTTCCTTTCAGTGGACCCGGGTCAAGAATACCCACATTCCG AAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGA GCTGAAGCGTGCTCACAAAAAGAAATACATGGAACTTGGAATCAGCCCAACGATCAAGAAAA TGCCTGGTGGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT CGGTTTTGCAGTGTCCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGAGTC GGGCTCCACCGGTTCGGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAAGAATTGGAAGC GCAAAATCATTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTCAGAAGGAC TACAACGTTGCTGTTCGCATCACTCCCCTAAAATACGCCCAGATTTGCCTCTGGATTCACGG GAACGATGCCAATTGTGCTTACGGC**TAA**CAGAGACCTGAAACAGGGCGGTGTATCATCTAAA TCACAGAGAAAACCAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTT GAACTCTGTCAATAGCATTTCAACATTTTTCAAAATCAGGAGATTTTCGTCCATTTAAAAAA TGTATAGGTGCAGATATTGAAACTAGGTGGGCACTTCAATGCCAAGTATATACTCTTCTTTA CATGGTGATGAGTTTCATTTGTAGAAAAATTTTGTTGCCTTCTTAAAAATTAGACACACTTT AAACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCC TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTGCATAGATAAA GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA CTCTGAGATGGATCCATTCAGCTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGTCT CAAAACTAATAACTGTTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTTAAAAA TGGGAGAAATAGTTTGTTCTATGAAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTT TAAGATCTCAAGTTTTTATTTAACTAATACTCAAAATATGGACTTTTCATGTATGCATAGGG AAGACACTTCACAAATTATGAATGATCATGTGTTGAAAGCCACATTATTTTATGCTATACAT CTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCTCTGATTAG TAATTTTAGATATGTCCTTTCCTAAAAATGAATAAAATTTATGAATATGA

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<MW: 47070, pI: 9.92, NX(S/T): 3

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YGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGILISPQHVLTAAHCVHDGKDYVKGSKKLRV
GLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGGRRRKKSGRGQRIAEGRPS
FQWTRVKNTHIPKGWARGGMGDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS
GFDNDRADQLVYRFCSVSDESNDLLYQYCDAESGSTGSGVYLRLKDPDKKNWKRKIIAVYSG
HQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site. amino acids 165-170

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT GTGACAGCAGGCAGAGGACCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCCGGCAAGG ATCCAAGCATGAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG GCCTGAGCAGCAGGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC TGCCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA AGTGCCAAGCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACT GTGGTTGCACTTCCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAAGGTCCTGATCACTT ATATCTGGAAACCAAAACCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA ATGGCTGGACCACTCACAGCAGATTTCATTGTCAAGATTCGTAACTCGGGCTCCGCTGACAG CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC CTTATGACCTCTACCATCCCCTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCC TCGTGTGGGGGGGCATCCAGAGCCGGGCAGTTTCCTGTGTGGAGGAGGACATCCAGGGGCA TGTCACTTCAGTGGAAGAGTGGAAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT GGCCAGGGCCTCAGATACCGTGTGGTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGG CTGTAGCCCAAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA AACCCAAAGAGAAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA GAAGAAGGAGCTGCTGTCAGAGGAGCCCTCG<u>TAA</u>GTTGTAAAAGCACAGACTGTTCTATA TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA AAAAAAAA

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AKGTTLVVELAPKVLDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVLKGPDHLYLETKTLQGTKGENSLSSTGTFL
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFPCS
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI
FDCPKWLAQEWSPCTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK
EKLPVEAKLPWFKQAQELEEGAAVSEEPS

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

CGGACGCGTGGGCGCGCTGCGGAACTCCCGTGGAGGGGCCGGTGGGCCCTCGGGCCTGAC AGATGCCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGGCGCTGTGGCCG GCCCGCCGGTTCGTGGGGCCCAGGGTCCAGCGCTGCGCAGAGGCGGGGACCCCGGCCTCAT GCACGGGAAGACTGTGCTGATCACCGGGGCGAACAGCGGCCTGGGCCGCGCCACGGCCGCCG GCGGCGGTCAGCTCCGCCGAGCTCCGCCAGGCCGCGAGTGCGGCCCAGAGCCTGGCGT CAGCGGGTGGCCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA TCTGGGGCACTTTCTACTCACCAATCTTCTCCTTGGACTCCTCAAAAGTTCAGCTCCCAGCA GGATTGTGGTAGTTTCTTCCAAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC AGTGAACAAAGCTATAATAAAAGCTTTTGTTATAGCCGGAGCAAACTGGCTAACATTCTTTT TACCAGGGAACTAGCCCGCCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTTGCATCCTG GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTC GGCCTCTTCACCTGAGGTAGAAGGAGTGTCAGGAAGATACTTTGGGGATTGTAAAGAGGAAG AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACTCTGGGATATCAGTGAAGTG ATGGTTGGCCTGCTAAAATAGAACAAGGAGTAAAAGAGCTGTTTATAAAACTGCATATCAG TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACTTGAAGAAAAAGAATTTTG ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTT GTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCAAGCATGGATGACATATTA ATATTTGTCAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTTTGTGTGGAAATTATCTGC CTGGTGTGTGCACACAAGTCTTACTTGGAATAAATTTACTGGTAC

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Important features:

Signal peptide:

amino acids 1-21

Short-chain alcohol dehydrogenase family protein amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGGCTCCCGGAGCCCAGCC CTTTCCTAACCCAACCCAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGAC ${\tt CCCAGCGTTACCATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCT}$ GCTCCTGGTAACTTGGGTTTTTACTCCTGTAACAACTGAAATAACAAGTCTTGCTACAGAGA ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGT CGTTTCAGTCAGATGTTGCATCCAATTTTTGAGGAAGCTTCCGATGTCATTAAGGAAGAATT TCCAAATGAAAATCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC AGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGAAG AGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAAG TGACCCCATTCAAGAAATTCGGGACTTAGCAGAAATCACCACTCTTGATCGCAGCAAAAGAA ATATCATTGGATATTTTGAGCAAAAGGACTCGGACAACTATAGAGTTTTTGAACGAGTAGCG AATATTTTGCATGATGACTGTGCCTTTCTTTCTGCATTTGGGGGATGTTTCAAAACCGGAAAG ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACT TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCCTCTT GTCCGAGAAATAACATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCCAGAATGAAGTAGCTCGGC AATTAATAAGTGAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT CCTCTTCTGCACATACAGAAAACTCCAGCAGATTGTCCTGTAATCGCTATTGACAGCTTTAG GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCCTGGAAAACTCAAGCAATTCG TATTTGACTTACATTCTGGAAAACTGCACAGAGAATTCCATCATGGACCTGACCCAACTGAT ACAGCCCCAGGAGAGCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTT**TAA**AAACTTG AAAAACAGTTTGTAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTA

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689</pre>

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46927, pI: 5.21, NX(S/T): 0

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GQRSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKDSDNYRVFERVANILH
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREI
TFENGEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH
IQKTPADCPVIAIDSFRHMYVFGDFKDVLIPGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG
EQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL

Important features:

Signal peptide:

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

ATTAAGGAAGAATTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATG GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

GCCCACGCGTCCGATGCCGTTCACGTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTTGATGAGCTGAAGACTGAT TACAAGAATCCTATAGACCAGTGTAATACCCTGAATCCCCTTGTACTCCCAGAGTACCTCAT CCACGCTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA TGCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGA GTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTACTACCTATATGGCATGATCTATGTTT TGGTGAGCTCT**TAG**AACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT TACTTTAAAAAATGACTCCTTATTTTTAAATGTTTCCACATTTTTTGCTTGTGGAAAGACTG TTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAAT GATTACCTCTGGTGTTGACAGGTTTGAACTTGCACTTCTTAAGGAACAGCCATAATCCTCTG AATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTTTATAGGAACTTGTA GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAAACTTCATGGGTTTCCTCATCTGTC ATGTCGATGATTATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGCTT GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTT AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG TACTACAGATTTTCAAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCCTTTAGT GCAATACAATAAAACTCTGAAATTAAGACTC

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330
<subunit 1 of 1, 144 aa, 1 stop
<MW: 16699, pI: 5.60, NX(S/T): 0

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FYLLAFFYYLYGMIYVLVSS</pre>

Important features:

Signal peptide:

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

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AATCCCCTTGTACTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGC

AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCTCTTGGCATATCATATTTTGGAGGTATA

TGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT

ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTT

TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACAACACACAGAAGAATT

GGTCCAGTTAAGTGCATGCAAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT

CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAAATG

CGGACGCGTGGGGGAAACCCTTCCGAGAAAACAGCAACAAGCTGAGCTGTGACAGAGGG GAACAAGATGCCGCCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGC TGCTGCTGACCATGGCCTTGGCCGGAGGTTCGGGGACCGCTTCGGCTGAAGCATTTGAC TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCACAC CTACCCTAAGGAAGAGGGTTGTACGCATGTCAGAGGGGTTGCAGGCTGTTTTCAATTTGTC AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA GAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC ATTCGCTGAACTGAGACAAGAACAACTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC TCTTCATGGACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCC AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA GCAAAATGTCCTATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGA GAAAGTGATGGCTTTTTAAGATGCCTCTCTTTAACTCTGGGTGGATTTTAACTACAACTCT TGTCCTCTCGGTGATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGC CTAAACAGATATCCAGCTTCTTCTCTTGTGGTTGTTAGATCTAAAACTGAAGATCATGAAGA AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAAT**TTA**AGCATTTTTCTTTT AAAAGACAAGTGTAATAGACATCTAAAATTCCACTCCTCATAGAGCTTTTTAAAATGGTTTCA TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

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<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

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ELRQEQLMSLMPKMHLLFPLTLVRSFWSDMMDSAQSFITSSWTFYLQADDGKIVIFQSKPEI
QYAPHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTTLVL
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG
PLPTKVNLAHSEI

Important features:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site.

amino acids 90-93

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCACACCTACCC
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTCGC
TGAACTGAGACAAGAACAACTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAA
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC
CCAACTGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTCGGGGACCG
CTTCGGCTGAAGCATTTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG
TTGACCTACCCCTTGCACACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG
CAGGCTGTTTTCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG
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GGTTGCCAGAATCAGCTGCCATTCGCTGAACTGAGACAACAACTTATGTCCCTGATGCC
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT
CCGC

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGCCGAGGCGGGCCTGGGAGGCGGCCCGGAGGT GGGGCGCCGCTGGGGCCGGCCCGCACGGCTTCATCTGAGGGCCACGGCCCGCGACCGAGC GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGGAGCTGCA**ATG**GGCCGCGGCTG GGGATTCTTGTTTGGCCTCCTGGGCGCCGTGTGGCTCCTCAGCTCGGGCCACGGAGAGGAGC AGCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGATTGT ACCTGTGATGTTGAAACCATTGATAGATTTAATAACTACAGGCTTTTCCCAAGACTACAAAA ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCCTTTCT GGAATGACATCAGCCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA GTTCCTGATGGAATTAAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC ATTCAGTCCCCTGAAGCTGAATATGTAGATTTGCTTCTTAATCCTGAGCGCTACACTGGTTA CAAGGGACCAGATGCTTGGAAAATATGGAATGTCATCTACGAAGAAAACTGTTTTAAGCCAC AGACAATTAAAAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACACT TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAAGAGCATTCTACAGACTTATATCTGG CCTACATGCAAGCATTAATGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAG AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTTGATGGAATTTTGACTGAA GGAGAAGGTCCAAGAAGGCTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTT ATCCAAAGTGTTACCATTCTTCGAGCGCCCAGATTTTCAACTCTTTACTGGAAATAAAATTC AGGATGAGGAAAACAAAATGTTACTTCTGGAAATACTTCATGAAATCAAGTCATTTCCTTTG CTTTCGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTTTGGTTGTTTTAAATGTC GTCTGTGGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG AAATTGATAGCAAATATGCCAGAAAGTGGACCTAGTTATGAATTCCATCTAACCAGACAAGA AATAGTATCATTATTCAACGCATTTGGAAGAATTTCTACAAGTGTGAAAGAATTAGAAAACT TCAGGAACTTGTTACAGAATATTCAT**TAA**AGAAAACAAGCTGATATGTGCCTGTTTCTGGAC AATGGAGGCGAAAGAGTGGAATTTCATTCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATTGTTTTAAGTAAACACATTTTT AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAAGTAATACTTTAATAATGTG AAAAAAAAAAAAAAAAAAAAAAAA

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<subunit 1 of 1, 468 aa, 1 stop

<MW: 54393, pI: 5.63, NX(S/T): 2

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NNLIEECEQAERLGAVDESLSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLLNPE
RYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAFY
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRRLKNLYFLYLI
ELRALSKVLPFFERPDFQLFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH
KLKEDFRLHFRNISRIMDCVGCFKCRLWGKLQTQGLGTALKILFSEKLIANMPESGPSYEFH
LTROEIVSLFNAFGRISTSVKELENFRNLLQNIH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 280-283 and 384-387

Amidation site.

amino acids 94-97

Glycosaminoglycan attachment site.

amino acids 20-23 and 223-226

Aminotransferases class-V pyridoxal-phosphate

amino acids 216-222

Interleukin-7 proteins

amino acids 338-343

GCTGGAAATATGGATGTCATCTACGAGAAACTGTTTTAAGCCACAGACAATTAAAAGACCTT
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTTACAGTTGGCTAGAA
GGTCTCTGTGTAGAAAAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA
ACATTACAGAATTTNAACAGCGATTTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG
CTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCATT
CTTNGAGCGCCCAGATTTTCAACTNTTTACTGGAAATAAAATTCAGGATGAGGNAAACAAAA
TGTTACTTTTGGAAAATACTTCATGAAAATCAAGTCATTTCCTTTTGCATTTTTGATGAGAATTCA
TTTTTTTGCTG

AGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC CGATCAGGCATGGAACTCCCCTTCGTCACTCACCTGTTCTTGCCCCTGGTGTTCCTGACAGG TCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTCCCAGGGCCACCAGAAG GCCCCTGGGATGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGG GGCCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTC ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTC ATGGTGAGC**TAA**GGAGAGGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAAGAGAA GTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCCTAGAAAGCAAA AGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT GCCCTCCCAAGCCTGGGAGTAACTATTTCCCCCATCCCCAGGCCTGTGCCCCTCTCTGGTCT CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCA GCCTCAGGGAAGCCTGGCACCCACTGCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTT CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCTGGCAAAGGG CCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAAGCTCCATGTTTCCTAACAGA TTCAGACTCCTGGCCAGGTGTGGTGGCCCACACCTGTAATTCTAGCACTTTGGGAGGCCAAG GTGGGCAGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACTCCAT CTCTACTAAAAAAAAAAAATACAAAAATTAGCTGGGTGCGCTAGTGCATGCCTGTAATCTC ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG AGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAAA AATAATAATAATAATTCAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGAG

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><subunit 1 of 1, 124 aa, 1 stop

><MW: 13352, pI: 5.99, NX(S/T): 1

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Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

AAAGTTACATTTTCTCTGGAACTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACTGAGTCTACCA **AATG**CAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGA AACAGTGTACTATTCTGTCGAATACCAGGGGGGGTACGAGAGCCTGTACACGAGCCACATCT GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATC ACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTG GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGCCTTTGTTGGCTTCATGCTGATCCTTGT GGTCGTGCCACTGTTCGTCTGGAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG TGGTCCTCCCAGACACCTTGAAAATAACCAATTCACCCCAGAAGTTAATCAGCTGCAGAAGG GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGAT $\tt CTCA{\color{red}{TAG}} GTTTGCGGAAGGGCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC$ ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC CTGGGAAAAGTGACTTCATCCCTTCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACC TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT GGCTTGGAGAGCCCACTTTCCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG TGTTGAGTTCACTTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT AGGTGACCTGGAGGAAGGTCACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC TGTTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA AAAAAAAAA

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033</pre>

<subunit 1 of 1, 311 aa, 1 stop

<MW: 35076, pI: 5.04, NX(S/T): 2

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SILKHPFNRNSTILTRPGMEITKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLVLALFAFVGFMLILV
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation site.

amino acids 40-43 and 134-137

Tissue factor proteins.

amino acids 92-119

Integrins alpha chain proteins

amino acids 232-262

GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAAGAGG AAAGACACAGAGAGAGAGAGAGAGAGAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG GCTGCTTTGGCATTTGGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCT GGAGGGACAGGGTCCCAGAAGGAGGGGGACAGAGGAGCTGAGAGAGGGGGGCAGGGCGTTGGG CAGGGGTCCCTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCTCGAGC GCTGGTACTCTGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG ACTGGTGGAGCTACAAGGATAATCTCCAGGGAAACTTCGTGCCAGGGCCTCCTTTCTGGGGC CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCCATTAAGGCTCAGCACTGGAGGAGAGA GTGGTCAATGTGTCTGGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAACTGCGGCTGCT GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTG AGGTGCAGCTCATTCACTTCAACCAGGAACTCTACGGGAATTTCAGCGCTGCCTCCCGCGGC $\tt CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCATTCCT$ CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTC TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC TCTCTCAGCACCCCGCCCTGCTCCGAGACTGTCACCTGGATCCTCATTGACCGGGCCCTCAA TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT TCCAGAGCCTCAGCGGTAACAGCCGGCCCCTGCAGCCCTTGGCCCACAGGGCACTGAGGGGC AACAGGGACCCCGGCACCCCGAGAGGCGCTGCCGAGGCCCCAACTACCGCCTGCATGTGGA $\mathtt{TGGTGTCCCCCATGGTCGC}$ \mathtt{TGA} $\mathtt{GACTCCCCTTCGAGGATTGCACCCGCCCGTCCTAAGCCTC}$ CCCACAAGGCGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGGACAGAATACTTA



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<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

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Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 177-199

N-glycosylation site.

amino acids 118-121, 170-173 and 260-263

Eukaryotic-type carbonic anhydrases proteins

amino acids 222-270, 128-164 and 45-92

GGCGCCTGGTTCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTCGCCGCCAGCCTCCGCCGCCGAGCCTC GTTCGTGTCCCCGCCCCTCGCTCCTGCAGCTACTGCTCAGAAACGCTGGGGCGCCCACCCTGGCAGACTAACGAA CGCAGAGGCGGAGGCTCGCGTATTCCTGCAGTCAGCACCCACGTCGCCCCCGGACGCTCGGTGCTCAGGCCCTTC $\tt ATCCTGAGGTCATTCATT \underline{ATG} \texttt{AAGTGTACCGCGCGGGGGGTGGCTCAGAGTAACCACAGTGCTGTTCATGGCTAGACCACAGTGCTGTTCATGGCTAGACCACAGTGCTGTTCATGGCTAGACCACAGTGCTGTTCATGGCTAGACCACAGTGCTGTTCATGGCTAGACCACAGTGCTGTTCATGGCTAGACCACAGTGCTGTTCATGGCTAGACCACAGTGCTGTTCATGGCTAGACCACAGTGCTGTTCATGGCTAGACCACAGTGCTGTTCATGGCTAGACCACAGTGCTGTTCATGGCTAGACTAGACTAGACTAACCACAGTGCTGTTCATGGCTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTAGACTA$ ${\tt GCAATTCCAGCCATGGTGGTTCCCAATGCCACTTTATTGGAGAAACTTTTTGGAAAAATACATGGATGAGGATGGT}$ GAGTGGTGGATAGCCAAACAACGAGGGAAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCAT AATAAATTACGAAGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA TTGGGAGCACACTGGGGAAGATATAGGCCCCCGACGTTTCATGTACAATCGTGGTATGATGAAGTGAAAGACTTT CAGGTCGTGTGGGCAACTAGTAACAGAATCGGTTGTGCCATTAATTTGTGTCATAACATGAACATCTGGGGGCAG ATATGGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAAGGGAAACTGGTGGGGCCATGCCCCTTACAAA CATGGGCGGCCCTGTTCTGCTTGCCCACCTAGTTTTGGAGGGGGCTGTAGAGAAAATCTGTGCTACAAAGAAGGG TCAGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATGAAATAGAACGACAGCAGTCACAAGTCCATGACACC CATGTCCGGACAAGATCAGATGATAGTAGCAGAAATGAAGTCATAAGCGCACAGCAAATGTCCCAAATTGTTTCT TGTGAAGTAAGATTAAGAGATCAGTGCAAAGGAACAACCTGCAATAGGTACGAATGTCCTGCTGTTTTGGAT AGTAAAGCTAAAGTTATTGGCAGTGTACATTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT ATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAAGCATTATTTCATCAAGTCCAATAGA AATGGTATTCAAACAATTGGCAAATATCAGTCTGCTAATTCCTTCACAGTCTCTAAAGTAACAGTTCAGGCTGTG ACTTGTGAAACAACTGTGGAACAGCTCTGTCCATTTCATAAGCCTGCTTCACATTGCCCAAGAGTATACTGTCCT CGTAACTGTATGCAAGCAAATCCACATTATGCTCGTGTAATTGGAACTCGAGTTTATTCTGATCTGTCCAGTATC TGCAGAGCAGCAGTACATGCTGGAGTGGTTCGAAATCACGGTGGTTATGTTGATGTAATGCCTGTGGACAAAAGA AAGACCTACATTGCTTCTTTCAGAATGGAATCTTCTCAGAAAGTTTACAGAATCCTCCAGGAGGAAAGGCATTC AGAGTGTTTGCTGTTGTGAAACTGAATACTTGGAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGA ATTTTGTATAAAACTGTAACATTACTGTACAGAGTACATCAACTATTTTCAGCCCAAAAAGGTGCCAAATGCATA TAAATCTTGATAAACAAAGTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAAATATAATGG TTTTAGAAATCCTGTGTTAAATATTGCTATATTTTCTTAGCAGTTATTTCTACAGTTAATTACATAGTCATGATT GTTCTACGTTTCATATATATATGGTGCTTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG TGTTAATTTAGGCATATAGAATATTAAATTCTGATATTGCACTTCTTATTTTATATAAAATAATCCTTTAATATC ATGAAAACATTCCTAGTGATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTTCTATGTACTGTTA AAATTGAGGTCACATATTTTCTTTTGTATCCTGGCAAATACTCCTGCAGGCCAGGAAGTATAATAGCAAAAAGTT ATATTGCCATATCATGGTACCTATAATGGTGATATATTTGTTTCTATGAAAAATGTATTGTGCTTTGATACTAAA

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<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

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Important features:

Signal peptide:

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

GCGGAGACAAGCGCAGAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG CAGCCGGAGCCAGCAGAGCCGGAAGGCGCCCCCGGCAGAAAAGCCGAGCAGAGCTGGGT GGCGTCTCCGGGCCGCTCCGACGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCG ACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT AGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTCTACGAA GAATAGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTGTGCAAAGGA TTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAG TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCT CCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTAA AAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGA GGAACATGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGC TTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG GTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCT GGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC CTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATA TTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACT TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA AACCTTCAAAGCATGTTTCCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT TTGTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGAT GACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCC CAGTATATGCCGCATTGTACTGCTGTTTATATGCTATGTACATGTCAGAAACCATTAGCAT TGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAA AAAAAAAAA

MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE

Signal sequence:

amino acids 1-34

GCCCAGGGACTGCTATGGCTTCCTTTGTTGTTCACCCCGGTCTGCGTCATGTTAAACTCCAATGTCCTCTGTG GTTAACTGCTCTTGCCATCAAGTTCACCCTCATTGACAGCCAAGCACAGTATCCAGTTGTCAACACAAATTATGG CAAAATCCGGGGCCTAAGAACACCGTTACCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCCTA TGCCTCACCCCCACTGGAGAGGGGGGTTTCAGCCCCCAGAACCCCCGTCCTCCTGGACTGGCATCCGAAATAC TACTCAGTTTGCTGCTGTGTGCCCCCAGCACCTGGATGAGAGATCCTTACTGCATGACATGCTGCCCATCTGGTT TACCGCCAATTTGGATACTTTGATGACCTATGTTCAAGATCAAAATGAAGACTGCCTTTACTTAAACATCTACGT GCCCACGGAAGATGGAGCCAACAAAGAAAAACGCAGATGATATAACGAGTAATGACCGTGGTGAAGACGAAGA TATTCATGATCAGAACAGTAAGAAGCCCGTCATGGTCTATATCCATGGGGGATCTTACATGGAGGGCACCGGCAA AGGGTTTTTAAGTACCGGTGACCAGGCAGCAAAAGGCAACTATGGGCTCCTGGATCAGATTCAAGCACTGCGGTG GATTGAGGAGAATGTGGGAGCCTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGGCTGGGGCCTC $\tt CTGTGTCAGCCTGTTGACCCTGTCCCACTACTCAGAAGGTCTCTTCCAGAAGGCCATCATTCAGAGCGGCACCGC$ ${\tt CCTGTCCAGCTGGGCAGTGAACTACCAGCCGGCCAAGTACACTCGGATATTGGCAGACAAGGTCGGCTGCAACAT}$ GCTGGACACCACGGACATGGTAGAATGCCTGCGGAACAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCCC GGCCACCTACCACATAGCCTTCGGGCCGGTGATCGACGGCGACGTCATCCCAGACGACCCCCAGATCCTGATGGA GCAAGGCGAGTTCCTCAACTACGACATCATGCTGGGCGTCAACCAAGGGGAAGGCCTGAAGTTCGTGGACGGCAT $\tt CGTGGATAACGAGGACGGTGTGACGCCCAACGACTTTGACTTCTCCGTGTCCAACTTCGTGGACAACCTTTACGG$ CTACCCTGAAGGGAAAGACACTTTGCGGGAGACTATCAAGTTCATGTACACAGACTGGGCCGATAAGGAAAACCC GCACGCGCAGTACGGCTCCCCCACCTACTTCTATGCCTTCTATCATCACTGCCAAAGCGAAATGAAGCCCAGCTG GGCAGATTCGGCCCATGGTGATGAGGTCCCCTATGTCTTCGGCATCCCCATGATCGGTCCCACCGAGCTCTTCAG TTGTAACTTTTCCAAGAACGACGTCATGCTCAGCGCCGTGGTCATGACCTACTGGACGAACTTCGCCAAAACTGG GTCCAAGTATAATCCCAAAGACCAGCTCTATCTGCATATTGGCTTGAAACCCAGAGTGAGAGATCACTACCGGGC AACGAAAGTGGCTTTCTGGTTGGAACTCGTTCCTCATTTGCACAACTTGAACGAGATATTCCAGTATGTTTCAAC AACCACAAAGGTTCCTCCACCAGACATGACATCATTTCCCTATGGCACCCGGCGATCTCCCGCCAAGATATGGCC AACCACCAAACGCCCAGCAATCACTCCTGCCAACAATCCCAAACACTCTAAGGACCCTCACAAAACAGGGCCTGA GGACACAACTGTCCTCATTGAAACCAAACGAGATTATTCCACCGAATTAAGTGTCACCATTGCCGTCGGGGCGTC GCTCCTCTTCCTCAACATCTTAGCTTTTGCGGCGCTGTACTACAAAAAGGACAAGAGGCGCCCATGAGACTCACAG GCGCCCCAGTCCCCAGAGAAACACCACAAATGATATCGCTCACATCCAGAACGAAGAGATCATGTCTCTGCAGAT GAAGCAGCTGGAACACGATCACGAGTGTGAGTCGCTGCAGGCACCACGACACTGAGGCTCACCTGCCCGCCAGA $\verb|CTACACCCTCACGCTGCGCCGGTCGCCAGATGACATCCCACTTATGACGCCAAACACCATCACCATGATTCCAAA||$ CACACTGACGGGGATGCAGCCTTTGCACACTTTTAACACCTTCAGTGGAGGACAAAACAGTACAAATTTACCCCA CGGACATTCCACCACTAGAGTATAGCTTTGCCCTATTCCCTTCCTATCCCTCTGCCCTACCCGCTCAGCAACAT AGAAGAGGGAAGGAAAGAGAAGGAAAGAGAGAGAGAAAGAAAGTCTCCAGACCAGGAATGTTTTTGTCCCACT AAGATCAACTTCTGACCCTGTGAAATGTGAGAAGTACACATTTCTGTTAAAATAACTGCTTTAAGATCTCTACCA $\tt CTCCAATCAATGTTTAGTGTGATAGGACATCACCATTTCAAGGCCCCGGGTGTTTCCAACGTCATGGAAGCAGCT$ CACACAATGGATGGCTCTCCTTAAGTGAAGAAAGAGTCAATGAGATTTTGCCCAGCACATGGAGCTGTAATCCAG AGAGAAGGAAACGTAGAAATTTATTATTAAAAGAATGGACTGTGCAGCGAAATCTGTACGGTTCTGTGCAAAGAG GTGTTTTGCCAGCCTGAACTATATTTAAGAGACTTTGT

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EDCLYLNIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI
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SLQAHDTLRLTCPPDYTLTLRRSPDDIPLMTPNTITMIPNTLTGMQPLHTFNTFSGGQNSTN
LPHGHSTTRV

Signal sequence:

amino acids 1-24

Transmembrane domains:

amino acids 189-204, 675-692

 $\tt GGGAAAG \underline{\textbf{ATG}} GCGGCGACTCTGGGACCCCTTGGGTCGTGGCAGCAGTGGCGGCGATGTTTGT$ CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTCTTTTTTTGGGGTCTGGGCAGGGGCCA CAGCAAGTCGGGGCGGGTCAAACGTTCGAGTACTTGAAACGGGAGCACTCGCTGTCGAAGCC CTACCAGGGTGTGGGCACAGGCAGTTCCTCACTGTGGAATCTGATGGGCAATGCCATGGTGA TGACCCAGTATATCCGCCTTACCCCAGATATGCAAAGTAAACAGGGTGCCTTGTGGAACCGG GTGCCATGTTTCCTGAGAGACTGGGAGTTGCAGGTGCACTTCAAAATCCATGGACAAGGAAA GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGC CTGTGTTTGGAAACATGGACAAATTTGTGGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT GAGGAGAAGCAGCAAGAGCGGGTATTCCCCTACATCTCAGCCATGGTGAACAACGGCTCCCT CAGCTATGATCATGAGCGGGATGGGCGGCCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC GCAATCTTCATTACGACACCTTCCTGGTGATTCGCTACGTCAAGAGGCATTTGACGATAATG ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGGAGTCCGCCTGCC CCGCGGCTACTACTTCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA TTTCCTTGAAGTTGTTTGAACTGACAGTGGAGAGAACCCCCAGAAGAGGAAAAGCTCCATCGA GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCGCC CCTGAGTGGCCTGGCCCTCTTCCTCATCGTCTTTTTCTCCCTGGTGTTTTTCTGTATTTGCCA TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA GCCCTCCTGCTGCCACCACTTTTGTGACTGTCACCCATGAGGTATGGAAGGAGCAGGCACTG GCCTGAGCATGCAGCCTGGAGAGTGTTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTG TCACTGGAGTTTTGAATGCAGGGACCCCGCATTCCCATGGTTGTGCATGGGGACATCTAACT $\mathtt{CTGGTCTGGGAAGCCACCCAGGGCAATGCTGCTGTGATGTGCCTTTCCCTGCAGTCC}$ TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGCCAAAATCACAGAAC AGAATTTCATAGCCCAGGCTGCCGTGTTGTTTGACTCAGAAGGCCCTTCTACTTCAGTTTTG TCTTCCCTGCCTTACCTTCCTTTCACTCCATTCATTGTCCTCTCTGTGTGCAACCTGAGCTG $\tt GGAAAGGCATTTGGATGCCTCTCTGTTGGGGCCTGGGGCTGCAGAACACACCTGCGTTTCAC$ TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTGTTCCCTAGCAT GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTG AAGTTTGGCTAAAGGTTGGTGTAAAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG GATTAGCTGTGCAACTGACCAGCTCCAGGTTTGATCAAACCAAAAGCAACATTTGTCATGTG GTCTGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCTGCTTAGCTGCATGTTTTGTAGT TACGATTTTTGGAATCCCACTTTGAGTGCTGAAAGTGTAAGGAAGCTTTCTTCTTACACCTT TGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCCTGGAAGAGTT CACTGTCATTGAGCAGCACAGCCTGAGTGCTGGCCTCTGTCAACCCTTATTCCACTGCCTTA TTTGACAAGGGGTTACATGCTCACCTTACTGCCCTGGGATTAAATCAGTTACAGGCCAG AGTCTCCTTGGAGGCCTGGAACTCTGAGTCCTCCTATGAACCTCTGTAGCCTAAATGAAAT ACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCCATGG

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><MW: 39711, pI: 8.70, NX(S/T): 1

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Signal sequence:

amino acids 1-38

Transmembrane domain:

amino acids 310-329

 $\tt CCGAGCCGGGCGCGCGGAGCGGGCCGGGCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT$ GACATGTTCCCGATTTGAGGTGAAACCATGAAGAGAAAATAGAATACTTAATA**ATG**CTTTTCCGCAACCGCTTCT CGACTCCTAAGAATGGAATGAGTAGCAAGAGTCGAAAGAGAATCATGCCCGACCCTGTGACGGAGCCCCCTGTGA CAGACCCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCCAGTGTGGCCGAGCGCAGCATGGAAGGTCATGCCC CGCATCATTTTAAGCTGGTCTCAGTGCATGTGTTCATTCGCCACGGAGACAGGTACCCACTGTATGTCATTCCCA AAACAAAGCGACCAGAAATTGACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCCAAAACTGGAAGCTTTCA TTAGTCACATGTCAAAAGGATCCGGAGCCTCTTTCGAAAGCCCCTTGAACTCCTTTGCCTCTTTACCCAAATCACC CATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTGCAGAACGGTCAGCTGCTGAGGGATA TCTATCTAAAGAAACACAAACTCCTGCCCAATGATTGGTCTGCAGACCAGCTCTATTTAGAGACCACTGGGAAAA GGCACCAGCCAAGTGCGCTGTTCTGCTCTGGAAGCTGCTATTGCCCGGTAAGAAACCAGTATCTGGAAAAGGAGC AGCGTCGTCAGTACCTCCTACGTTTGAAAAACAGCCAGCTGGAGAAGACCTACGGGGAGATGGCCAAGATCGTGG ATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTTCTGCCACAATGTCAGCT TTCCCTGTACCAGAAATGGCTGTTGTTGACATGGAGCACTTCAAGGTAATTAAGACCCATCAGATCGAGGATGAAA GGGAAAGACGGGAGAAGAATTGTACTTCGGGTATTCTCTCCTGGGTGCCCACCCCATCCTGAACCAAACCATCG GCCGGATGCAGCGTGCCACCGAGGGCAGGAAAGAAGAGGCTCTTTGCCCTCTACTCTGCTCATGATGTCACTCTGT ${\tt CACCAGTTCTCAGTGCCTTTGGGCCTTTCAGAAGCCAGGTTCCCAAGGTTTGCAGCCAGGTTGATCTTTGAGCTTT}$ GGCAAGACAGAGAAAAGCCCAGTGAACATTCCGTCCGGATTCTTTACAATGGCGTCGATGTCACATTCCACACCT CTTTCTGCCAAGACCACACAGCGTTCTCCCAAGCCCATGTGCCCGCTTGAAAACTTGGTCCGCTTTGTGAAAA ${\tt GGGACATGTTTGTAGCCCTGGGTGGCAGTGGTACAAATTATTATGATGCATGTCACAGGGAAGGATTC} {\color{red}{\bf TAA}} {\tt AAGG}$ TATGCAGTACAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAAGGTCCACTTCTAGTTTTGTCTGTTAC AAGCACATTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAAATGGCCAGTTCACAGAGGAATAGAAGGTACTT TATCATAGCCAGACTTCGCTTAGAATGCCAGAATAATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCAC ${\tt TCTTCTGGCCTGCCCCATGTTACTATGTGATGGAACCAGCACACCTCAACCAAAATTTTTTTAATCTTAGACATT}$ TTTACCTTGTCCTTGTTAAGAATTTCTTGAAGTGATTTATCTAAAATAAAGGTTGGCAAACTTTTTCTGTAAAGG GCCAGATTGTAAATATTTCAGACTGTGTGGACCAAAAGGCCACATACAGTCTCTGTCATAACTACTCAACTCTGT TTCTGAAGCAGGAAAGCCACCACAGACAGTACATAAAGGAATATGTGTAGCTGGGTTCCCAGGCCAGACAAAACA GATGGTGACCAGACTTGGCCCCTGGGCTGTAGTTTGCTGACCCCTCATCTAAAAAATAGGCTATACTACAATTGC ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGAATTATTCAATGGTTCCTCCAGTAACTTCTGCTAGAAACA AACTGATTAGAAGAATACTTGATGTTTATGATGATTGTGGTACAAGATAGTTTTAAGTATGTTCTAAATATTTGT CTGCTGTAGTCTATTTGCTGTATATGCTGAAATTTTTGTATGCCATTTAGTATTTTTATAGTTTAGGAAAATATT TTCTAAGACCAGTTTTAGATGACTCTTATTCCTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAG GAGGCTAGAAGATGAATTCAGGCACTTTCTTCCAATAAAACTAATTATGGCTCATTCCCTTTGACAAGCTGTAGA AGAACTTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATATTAGAAGCAATTATAATTACATCTG TGATTTCTGAACTAATGGTGCTAATTCAGAGAAATGGAAAGTGAAAGTGAGATTCTCTGTTGTCATCGGCATTCC

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><subunit 1 of 1, 480 aa, 1 stop

><MW: 55240, pI: 9.30, NX(S/T): 2

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KHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP
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TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELF
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Signal sequence:

amino acids 1-18

GCTATTTAAGAGATAAAACGAAATATCCTTTCTGGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC GCCGCTGTTCACCAATCGGGGAGAAAAGCGGAGATCCTGCTCGCCTTGCACGCGCCTGAAGCACAAAGCAGAT AGCTAGGAATGAACCATCCCTGGGAGTATGTGGAAACAACGGAGGAGCTCTGACTTCCCAACTGTCCCATTCTAT GGGCGAAGGAACTGCTCCTGACTTCAGTGGTTAAGGGCAGAATTGAAAATAATTCTGGAGGAAGATAAGA**ATG**AT TCCTGCGCGACTGCACCGGGACTACAAAGGGCTTGTCCTGCTGGGAATCCTCCTGGGGACTCTGTGGGAGACCGG ATGCACCCAGATACGCTATTCAGTTCCGGAAGAGCTGGAGAAAGGCTCTAGGGTGGGCGACATCTCCAGGGACCT GGGGCTGGAGCCCCGGGAGCTCGCGGAGCGCGGAGTCCGCATCATCCCCAGAGGTAGGACGCAGCTTTTCGCCCT GAATCCGCGCAGCGGCAGCTTGGTCACGGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCAAGTG TCAATTAAATCTAGACATTCTGATGGAGGATAAAGTGAAAATATATGGAGTAGAAGTAGAAGTAAGGGACATTAA CGACAATGCGCCTTACTTTCGTGAAAGTGAATTAGAAATAAAAATTAGTGAAAATGCAGCCACTGAGATGCGGTT CCCTCTACCCCACGCCTGGGATCCGGATATCGGGAAGAACTCTCTGCAGAGCTACGAGCTCAGCCCGAACACTCA CGAAGAAAAGGCTGCTCACCACCTGGTCCTTACGGCCTCCGACGGGGGCGACCCGGTGCGCACAGGCACCGCGCG CATCCGCGTGATGGTTCTGGATGCGAACGACACGCACCAGCGTTTGCTCAGCCCGAGTACCGCGCGAGCGTTCC GGAGAATCTGGCCTTGGGCACGCTGCTTGTAGTCAACGCTACCGACCCTGACGAAGGAGTCAATGCGGAAGT GAGGTATTCCTTCCGGTATGTGGACGACAAGGCGGCCCAAGTTTTCAAACTAGATTGTAATTCAGGGACAATATC TTCTGCGCGAGCCAAAGTCCTGATCACTGTTCTGGACGTGAACGACAATGCCCCAGAAGTGGTCCTCACCTCTCT CGCCAGCTCGGTTCCCGAAAACTCTCCCAGAGGGACATTAATTGCCCTTTTAAATGTAAATGACCAAGATTCTGA GGAAAACGGACAGGTGATCTGTTTCATCCAAGGAAATCTGCCCTTTAAATTAGAAAAATCTTACGGAAATTACTA TAGTTTAGTCACAGACATAGTCTTGGATAGGGAACAGGTTCCTAGCTACAACATCACAGTGACCGCCACTGACCG GGGAACCCCGCCCTATCCACGGAAACTCATATCTCGCTGAACGTGGCAGACACCAACGACAACCCGCCGGTCTT CGACCCCGACTGTGAAGAGACGCCCAGATCACTTATTCCCTGGCTGAGAACACCATCCAAGGGGCAAGCCTATC GTCCTACGTGTCCATCAACTCCGACACTGGGGTACTGTATGCGCTGAGCTCCTTCGACTACGAGCAGTTCCGAGA $\tt CTTGCAAGTGAAGTGATGGCGCGGGACAACGGGCACCCGCCCCTCAGCAGCAACGTGTCGTTGAGCCTGTTCGT$ GGCTCCCCGCTCCGCAGAGCCCGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCCGGCCAGAACGC $\tt CCTCGAGTCTCCAGCTAACTCTGAAACCTCAGACCTCACTCTGTACCTGGTGGTAGCGGTGGCCGCGGTCTCCTG$ CGTCTTCCTGGCCTTCGTCATCTTGCTGCTGCGCGCTCAGGCTGCGCGCTGCCACAAGTCACGCCTGCTGCAGGC CTATTCCCACGAGGTTTCCCTCACCACGGACTCGCGGAAGAGTCACCTGATCTTCCCCCAGCCCAACTATGCAGA CATGCTCGTCAGCCAGGAGAGCTTTGAAAAAAGCGAGCCCCTTTTGCTGTCAGGTGATTCGGTATTTTCTAAAGA $\tt TGGAGTGCAGCGGTACGATCATAGCTCACTGCGGCCTCAAACTCCTAGGCTCAAGCAATTATCCCACCTTTGCCT$ $\tt CTATCTATCTATCTATCTATCTTGTACAGACGGGAGTCTCACGCCTGTAATCCCAGTACTTTGGGAGGC$ TGCTTTAACCTGGGAGGTTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCCTGGGCAACAAGAGTG AAACTCTATCTCA

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306</pre>

><subunit 1 of 1, 916 aa, 1 stop

><MW: 100204, pI: 4.92, NX(S/T): 4

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GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVR
DINDNAPYFRESELEIKISENAATEMRFPLPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA
DGSKYPELVLKRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAFAQPEYR
ASVPENLALGTQLLVVNATDPDEGVNAEVRYSFRYVDDKAAQVFKLDCNSGTISTIGELDHE
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLNVN
DQDSEENGQVICFIQGNLPFKLEKSYGNYYSLVTDIVLDREQVPSYNITVTATDRGTPPLST
ETHISLNVADTNDNPPVFPQASYSAYIPENNPRGVSLVSVTAHDPDCEENAQITYSLAENTI
QGASLSSYVSINSDTGVLYALSSFDYEQFRDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDN
APEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVDRDSGQNAWLSYRLLKASEPGLFSVG
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADSIPQVLADLGSLESPA
NSETSDLTLYLVVAVAAVSCVFLAFVILLLALRLRRWHKSRLLQASGGGLTGAPASHFVGVD
GVQAFLQTYSHEVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGL
IEVSLYQIFFLFFFNCSVSQAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRDYRCKPPTVCLS
IYLSIYLSIYLSIYLLISCTDGSLTPVIPVLWEAEAGGSPEVGSLRPA

Signal sequence:

amino acids 1-30

Transmembrane domains:

amino acids 693-711, 809-823, 869-888

CCCAGGCTCTAGTGCAGGAGGAGGAGGAGGAGGAGGAGGTGGAGATTCCCAGTTAAAAG GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA TCAGTAGGTGACCCCGCCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCCGACCTCGT ACAGGAGGACAAGGTGCTGGGGGGTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAGGTGGCAACTGGGTCCTT ACAGCTGCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCTACAACA GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG CACCGTCTCAGGCTGGGGCACTGTCACCAGTCCCCGAGAGAATTTTCCTGACACTCTCAACT GTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA GATGGCATGGTCTGTGCAGGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG CCCCCTGGTGTGTGATGGTGCACTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC ${\tt ATAGGCAGCAAGGGC} \underline{{\tt TGA}} {\tt TTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCT}$ CTGGTTC

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336</pre>

<subunit 1 of 1, 260 aa, 1 stop

<MW: 28048, pI: 7.87, NX(S/T): 1

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Important Features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCCCCGGCCCCGC CGCGCCGCCCACGCCCAACCCCGGCCCGCGCCCCTAGCCCCGGCCCGGGCCCGCGCCCGCGCCCGC CCCCGGCCGGCGGGGAACCGGGCGGATTCCTCGCGCGTCAAACCACCTGATCCCATAAAAC ATTCATCCTCCGGCGGCCGCGCTGCGAGCGCCCGCCAGTCCGCCGCCGCCGCCCTCG TGCGGACCCGCCGCGGGGAGACGGCGCCCCCGAAACGACTTTCAGTCCCCGACGCGC CTGTGGCTGCAGGCCTGCAGGTGCCAGCCCCATGCCCAGGTGCCTATGCTACAATGA GCCCAAGGTGACGACAAGCTGCCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTG CTGCCAGCCAGCGCATCTTCCTGCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC CGTGCCTGCCGCAACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCGAATTGATGC GGCTGCCTTCACTGGCCCTGCCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC GGTCTGTGGACCCTGCCACATTCCACGGCCTGGGCCGCCTACACACGCTGCACCTGGACCGC TGCGGCCTGCAGGAGCTGGGCCCGGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTA CCTGCAGGACAACGCGCTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCA CACACCTCTTCCTGCACGGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGTGGGCTG CACAGCCTCGACCGTCTCCTACTGCACCAGAACCGCGTGGCCCATGTGCACCCGCATGCCTT CCGTGACCTTGGCCGCCTCATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCA CTGAGGCCCTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG TGTGACTGCCGGGCACGCCCACTCTGGGCCTGCTGCAGAAGTTCCGCGGCTCCTCCTCCGA GGTGCCTGCAGCCTCCCGCAACGCCTGGCTGGCCGTGACCTCAAACGCCTAGCTGCCAATG ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACC ACTGGAGCCTGGAAGACCAGCTTCGGCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTG ACAGCCGGCGGGCAACGGCTCTGGCCCACGGCACATCAATGACTCACCCTTTGGGACTCTG CCTGGCTCTGCTGAGCCCCCGCTCACTGCAGTGCGGCCCGAGGGCTCCGAGCCACCAGGGTT CCCCACCTCGGGCCCTCGCCGGAGGCCAGGCTGTTCACGCAAGAACCGCACCCGCAGCCACT GCCGTCTGGGCCAGGCAGCCGGGGGTGGCGGGACTGGTGACTCAGAAGGCTCAGGTGCC CTACCCAGCCTCACCTGCAGCCTCACCCCCTGGGCCTGGCGCTGGTGCTGTGGACAGTGCT $\mathtt{TGGGCCCTGC}$ GGGGTCTCTCCACGCCGCCAAGCCAGCCGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAG GCATTTTATTTTACTTGTGTAAAAATATCGGACGACGTGGAATAAAGAGCTCTTTTCTTAAA AAAA

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184</pre>

><subunit 1 of 1, 473 aa, 1 stop

><MW: 50708, pI: 9.28, NX(S/T): 6

MKRASAGGSRLLAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI FLHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAAFTGLALLEQLDLSDNAQLRSVDPA TFHGLGRLHTLHLDRCGLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH GNRISSVPERAFRGLHSLDRLLLHQNRVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAP LRALQYLRLNDNPWVCDCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCA VATGPYHPIWTGRATDEEPLGLPKCCQPDAADKASVLEPGRPASAGNALKGRVPPGDSPPGN GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA GSGGGTGDSEGSGALPSLTCSLTPLGLALVLWTVLGPC

Important features:

Signal peptide:

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCCTCTGGAGAGGACTAC TCACTGGCATATTTCTGAGGTATCTGTAGAATAACCACAGCCTCAGATACTGGGGACTTTAC AGTCCCACAGAACCGTCCTCCCAGGAAGCTGAATCCAGCAAGAACAATGGAGGCCAGCGGGA AGCTCATTTGCAGACAAAGGCAAGTCCTTTTTTCCTTTTCTCCTTTTTGGGCTTATCTCTGGCG GGCGCGGCGGAACCTAGAAGCTATTCTGTGGTGGAGGAAACTGAGGGCAGCTCCTTTGTCAC CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGGCGGGGGGTTAGGGTTG TTTCCAGAGGGAACAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTTGTTGCTAAAT GAGAAATTGGACCGTGAGGATCTGTGCGGTCACACAGAGCCCTGTGTGCTACGTTTCCAAGT GTTGCTAGAGAGTCCCTTCGAGTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCCTCCTGGG ACTACGTTTCCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAACTA TATAATCAGCCCCAACTCCTATTTTCGGGTCCTCACCCGCAAACGCAGTGATGGCAGGAAAT ACCCAGAGCTGGTGCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAACA CTCACAGCACTGGATGGTGGCTCTCCGCCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT CCTGGATGTCAACGATAATGCCCCTGAATTTGAGCAGCCTTTCTATAGAGTGCAGATCTCTG AGGACAGTCCGGTAGGCTTCCTGGTTGTGAAGGTCTCTGCCACGGATGTAGACACAGGAGTC AACGGAGAGATTTCCTATTCACTTTTCCAAGCTTCAGAAGAGATTGGCAAAACCTTTAAGAT CAATCCCTTGACAGGAGAAATTGAACTAAAAAAACAACTCGATTTCGAAAAAACTTCAGTCCT ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTTCTGGAAAATGCACCGTTCTGATT CAAGTGATAGATGTGAACGACCATGCCCCAGAAGTTACCATGTCTGCATTTACCAGCCCAAT ACCTGAGAACGCGCCTGAAACTGTGGTTGCACTTTTCAGTGTTTCAGATCTTGATTCAGGAG AAAATGGGAAAATTAGTTGCTCCATTCAGGAGGATCTACCCTTCCTCCTGAAATCCGCGGAA AACTTTTACACCCTACTAACGGAGAGACCACTAGACAGAGAAAGCAGAGCGGAATACAACAT CACTATCACTGTCACTGACTTGGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC TGATCGCCGATGTCAATGACAACGCTCCCGCCTTCACCCCAAACCTCCTACACCCTGTTCGTC CACCAACGCCCAGGTCACCTACTCGCTGCTGCCGCCCCAGGACCCGCACCTGCCCCTCACAT CCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTCGCCCTCAGGTCTCTGGACTACGAG GCCCTGCAGGGGTTCCAGTTCCGCGTGGGCGCTTCAGACCACGGCTCCCCGGCGCTGAGCAG CGAGGCGCTGGTGCGGGTGCTGGACGCCAACGACAACTCGCCCTTCGTGCTGTACC CTGGTGACCAAGGTGGTGGCGGTGGACGCCGACTCGGGCCAGAACGCCTGGCTGTCGTACCA GCTGCTCAAGGCCACGGAGCTCGGTCTGTTCGGCGTGTGGGCGCACAATGGCGAGGTGCGCA CCGCCAGGCTGCTGAGCGAGCGCGACGCCCAAGCACAGGCTGGTGCTGGTCAAGGAC AATGGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCCTGGTGGACGGCTTCTC CCAGCCTACCTGCCTCTCCCGGAGGCGGCCCCGACCCAGGCCCAGGCCGACTTGCTCACCG TCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTTCCTTTTCGGTGCTCCTGTTC GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCCTCGGTGGGTCGCTGCTTGGTGCCCGA GGGCCCCCTTCCAGGGCATCTTGTGGACATGAGCGGCACCAGGACCCTATCCCAGAGCTACC AGTATGAGGTGTGTCTGGCAGGAGGCTCAGGGACCAATGAGTTCAAGTTCCTGAAGCCGATT ATCCCCAACTTCCCTCCCCAGTGCCCTGGGAAAGAAATACAAGGAAATTCTACCTTCCCCAA ${\tt TAACTTTGGGTTCAATATTCAG}$ ${\tt TGACTTGACTTTTACATTCCATAGGTATTTTATTT}$ TTACTCTTGATTTTTCTCATGTTCTTTCTCCCTTTGTTTTAAAGTGAACATTTACCTTTATT CCTGGTTCTT

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<subunit 1 of 1, 798 aa, 1 stop

<MW: 87552, pI: 4.84, NX(S/T): 5

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IDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNAPEFEQPFY
RVQISEDSPVGFLVVKVSATDVDTGVNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPENAPETVVALFSVS
DLDSGENGKISCSIQEDLPFLLKSAENFYTLLTERPLDRESRAEYNITITVTDLGTPMLITQ
LNMTVLIADVNDNAPAFTQTSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLLPPQDP
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELGLFGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAQ
ADLLTVYLVVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMSGTRT
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNFPPQCPGKEIQGNSTFPNNFGFNIQ

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 685-712

Cadherins extracellular repeated domain signature.

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

ATP/GTP-binding site motif A (P-loop).

amino acids 285-292

N-glycosylation site.

amino acids 418-421, 436-439, 567-570 and 786-789

ACCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCGCGTCCGCGCGTAGCCGTGC GCCGATTGCCTCTCGGCCTGGGCATGGTCCCGGCTGCCGGTCGACGACCGCCCCGCGTCAT GCGGCTCCTCGGCTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTGG AGGTTGCAGAGGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCCTCTCCAGGTG GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGCCAGC AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG TGATTCCTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTCTGGATGGCGCTGG AGCACACTTCCCTGACAGAGAGAGGGGGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTCACAGGACCT TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCCTGTTTTACACCCCGTGGT GCCGCTTTTCTGCCAGTTTGGCCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT CACTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC TGTTCCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATACAGATC GAACACTGGAAACACTGAAAATCTTCATTTTTAATCAGACAGGTATAGAAGCCAAGAAGAAT GTGGTGGTAACTCAAGCCGACCAAATAGGCCCTCTTCCCAGCACTTTGATAAAAAGTGTGGA $\tt CTGAGAGTATTCGGTGGCTAATTCCAGGACAAGAGCAGGAACATGTGGAG{\bf TAG}{\bf TGATGGTCT}$ GAAAGAAGTTGGAAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA CATTTTCTCCAGTGACGTGTTGACTTGAAACTTCAGGCAGATTAAAAGAATCATTTGTTGAA CAACTGAATGTATAAAAAATTATAAACTGGTGTTTTTAACTAGTATTGCAATAAGCAAATGC AAAAATATTCAATAG

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><subunit 1 of 1, 360 aa, 1 stop

><MW: 39885, pI: 4.79, NX(S/T): 7

MVPAAGRRPPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEE ELLHDPMGQDRAAEEANAVLGLDTQGDHMVMLSVIPGEAEDKVSSEPSGVTCGAGGAEDSRC NVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE NFTLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS QHSSLSTRFGTVAVPNILLFQGAKPMARFNHTDRTLETLKIFIFNQTGIEAKKNVVVTQADQ IGPLPSTLIKSVDWLLVFSLFFLISFIMYATIRTESIRWLIPGQEQEHVE

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 321-340

Homologous region to dilsufide isomerase

amino acids 212-302

N-glycosylation site.

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281 and 293-296

Thioredoxin domain

amino acids 211-227

CCCGGCTCCGCTCTGCCCCCTCGGGGTCGCGCCCACGATGCTGCAGGGCCCTGGCT TTTGGCCAGCCCGACTTCTCCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCAACCTGCTGGGCCACGAGACCA TGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGĆAGTGCCACCCG GACACCAAGAAGTTCCTGTGCTCGCTCTTCGCCCCCGTCTGCCTCGATGACCTAGACGAGAC CATCCAGCCATGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGCCCCGGTCATGTCCG CCTTCGGCTTCCCCTGGCCCGACATGCTTGAGTGCGACCGTTTCCCCCAGGACAACGACCTT TGCATCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG ATTTTGCACTGAAAATAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAAATCATC CTGGAGACCAAGAGCATTTACAAGCTGAACGGTGTCCGAAAGGGACCTGAAGAA ATCGGTGCTGTGGCTCAAAGACAGCTTGCAGTGCACCTGTGAGGAGATGAACGACATCAACG CGCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGC<u>TA</u> **G**TCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTTCTGCTCC GGGATCTCAGCTCCCGTTCCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTTCCTGAGTTATAAGGCCACAGGAGTG GATAGCTGTTTTCACCTAAAGGAAAAGCCCACCCGAATCTTGTAGAAATATTCAAACTAATA AAATCATGAATATTTTAA

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><subunit 1 of 1, 295 aa, 1 stop

><MW: 33518, pI: 7.74, NX(S/T): 0

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Important features:

Signal peptide:

amino acids 1-20

Cysteine rich domain, homolgous to frizzled N terminus amino acids 6-153

CCCTGTGCGCGCACCGGGCCACCTACGCGCGCCGCTGGGTGTTCCTGCTCGCGATC AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT TGCTGAGGACTTGGTCCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTCGGGCTCCGTGCGGCC ACCATCCTGGGTGCGTGAACTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT TGTTGGGACCCAAAACCCATTTGCCTTCCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC AGAGCCTGGTCATCTTCTCCCAGCCAAGCTGGCTGCCTTGTGGTTCCCAGAGCACCAGCGA GCCACGGCCACATGCTCGCCACCATGTCGAACCCTCTGGGCGTCCTTGTGGCCAATGTGCT GTCCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATACCATCC CTGCTGGCGTCGTCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCCACCCCG CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCCTGGATGGGCTCAAGCTGCAGCT CATGTGGAACAAGGCCTATGTCATCCTGGCTGTGTGCTTGGGGGGAATGATCGGGATCTCTG CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCC GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCCTA TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG ${\tt CCTGCGTGCCCTTTGCCCTGGTGTCCCAGCTGCAGGGACAGACCCTTGCCCTGGCTGCCACC}$ TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTCGA GTGTTCCTTCCCGTGGGGGGGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCCTTG TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCGG CCTGTGCACCTTCTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGGCGCCTGC AGGCCGAGTCTGGGGAGCCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG GGTGTGGACCGAGGGGGGGCAGGAAGGGCTGGGGTCCTGGGGCCCAGCACGGCGACTCCGGA GCCACCGAGCGACTCCCCGTGCGCAAGGCCCAGCACCGACGCGCCCCTCCCGCCCCGGC AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTT CTCCTCCCGTGGGTGATCACG**TAG**CTGAGCGCCTTGTAGTCCAGGTTGCCCGCCACATCGA CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

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><subunit 1 of 1, 560 aa, 1 stop

><MW: 58427, pI: 6.86, NX(S/T): 2

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PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQRATANMLATMSNPLGVLVANVLSPVLV
KKGEDIPLMLGVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA
YVILAVCLGGMIGISASFSALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK
HFTEATKIGLCLFSLACVPFALVSQLQGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV
GEGAATGMIFVLGQAEGILIMLAMTALTVRRSEPSLSTCQQGEDPLDWTVSLLLMAGLCTFF
SCILAVFFHTPYRRLQAESGEPPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG
ASLEDPRGPGSPHPACHRATPRAQGPAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268, 280-300, 318-337, 341-357, 375-387, 420-441

N-glycosylation site.

amino acids 40-43 and 43-46

Glycosaminoglycan attachment site.

amino acids 468-471

GTCCCACATCCTGCTCAACTGGGTCAGGTCCCTCTTAGACCAGCTCTTGTCCATCATTTGCTGAAGTGGACCAAC TAGTTCCCCAGTAGGGGGTCTCCCCTGGCAATTCTTGATCGGCGTTTTGGACATCTCAGATCGCTTCCAATGAAGA TGGCCTTGCCTTGGGGTCCTGCTTGTTTCATAATCATCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGG AAGGAGCACGGGGCTGATCAAGCCATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAAGAACTCTAGTGGTT ${\tt TCTGAATCTAGCCCACTTGGCGGTAAGC} {\tt ATG} {\tt ATG} {\tt CAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGGTGG}$ CTACTTATTTCTTTTAGGGGATTGTCAGGAGGTGACCACTCTCACGGTGAAATACCAAGTGTCAGAGGAAGTGCC ATCTGGTACAGTGATCGGGAAGCTGTCCCAGGAACTGGGCCGGGAGGAGGGGAGGCAAGCTGGGGCCGCCTT GGCTCTGATCCATGTGGAGATCCAAGTGCTGGACATCAATGACCACCAGCCACGGTTTCCCAAAGGCGAGCAGGA GCTGGAAATCTCTGAGAGCGCCTCTCTGCGAACCCGGATCCCCCTGGACAGAGCTCTTGACCCAGACACAGGCCC TAACACCTGCACACCTACACTCTGTCTCCCAGTGAGCACTTTGCCTTGGATGTCATTGTGGGCCCTGATGAGAC CTATGACAATGGGAACCCCCCCAAGTCAGGTACCAGCTTGGTCAAGGTCAACGTCTTGGACTCCAATGACAATAG CCCTGCGTTTGCTGAGAGTTCACTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAAACT GACCGCCACAGACCCTGACCAAGGCCCCAATGGGGAGGTGGAGTTCTTCCTCAGTAAGCACATGCCTCCAGAGGT GCTGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTCATTCTGCGTCGACCTCTAGACTATGAAAAGAACCC TGCCTACGAGGTGGATGTTCAGGCAAGGGACCTGGGTCCCAATCCTATCCCAGCCCATTGCAAAGTTCTCATCAA GGTTCTGGATGTCAATGACAACATCCCAAGCATCCACGTCACATGGGCCTCCCAGCCATCACTGGTGTCAGAAGC TCTTCCCAAGGACAGTTTTATTGCTCTTGTCATGGCAGATGACTTGGATTCAGGACACAATGGTTTGGTCCACTG CACACTGGACAGAGAGCAGTGGCCCAAATATACCCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATC AGCCAAGAAACAGCTCAGCATTCAGATCAGTGACATCAACGACAATGCACCTGTGTTTTGAGAAAAGCAGGTATGA AGTCTCCACGCGGGAAAACAACTTACCCTCTCTCACCTCATTACCATCAAGGCTCATGATGCAGACTTGGGCAT TAATGGAAAAGTCTCATACCGCATCCAGGACTCCCCAGTTGCTCACTTAGTAGCTATTGACTCCAACACAGGAGA GGTCACTGCTCAGAGGTCACTGAACTATGAAGAGATGGCCGGCTTTGAGTTCCAGGTGATCGCAGAGGACAGCGG GCAACCCATGCTTGCATCCAGTGTCTCTGTGTGGGTCAGCCTCTTGGATGCCAATGATAATGCCCCAGAGGTGGT ${\tt CCAGCCTGTGCTCAGCGATGGAAAAGCCAGCCTCTCCGTGCTTGTGAATGCCTCCACAGGCCACCTGCTGGTGCC}$ CATCGAGACTCCCAATGGCTTGGGCCCAGCGGGCACTGACACCCTCCACTGGCCACTCACAGCTCCCGGCCATT CCTTTTGACAACCATTGTGGCAAGAGATGCAGACTCGGGGGCCAAATGGAGCCCCTCTACAGCATCCGCAATGG AAATGAAGCCCACCTCTTCATCCTCAACCCTCATACGGGGCAGCTGTTCGTCAATGTCACCAATGCCAGCAGCCT ${\tt CATTGGGAGTGAGTGGAGATAGTAGTAGAGGACCAGGGAAGCCCCCCTTACAGACCCGAGCCCTGTT}$ GAGGGTCATGTTGTCACCAGTGTGGACCACCTGAGGGACTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTCGAT GCTGACGGTGATCTGCCTGGCTGTACTGTTGGGCATCTTCGGGTTGATCCTGGCTTTGTTCATGTCCATCTGCCG GACAGAAAAGAAGGACAACAGGGCCTACAACTGTCGGGAGGCCGAGTCCACCTACCGCCAGCAGCCCAAGAGGCC CCACCTCACCCGACCCTGTACAGGACGCTGCGTAATCAAGGCAACCAGGGAGCACCGGCGGAGAGCCGAGAGGT GCTGCAAGACACGGTCAACCTCCTTTTCAACCATCCCAGGCAGAGGAATGCCTCCCGGGAGAACCTGAACCTTCC TGGAGACCAGGGCAGTGAGGAGCCCCACAGAGGCCACCAGCCTCCTCTGCAACCCTGAGACGGCAGCGACATCT TGCCTTCGCCGAGCGGAACCCCGTGGAGGAGCTCACTGTGGATTCTCCTCCTGTTCAGCAAATCTCCCAGCTGCT AGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGAAGCAACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCC CACCAACTACCGTGACAATGTGATCTCCCCGGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGTTCGG ${\tt CAAGGCAGAGGCAGAGCCCAACAGGCACGAGGCTGGCCAGCACCTTTGTCTCGGAGATGAGCTCACT}$ GCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCCGTGGAGGCCGCCTCCGAGGCGCTGCGGCGGCTCTCGGT CTGCGGGAGGACCCTCAGTTTAGACTTGGCCACCAGTGCAGCCTCAGGCATGAAAGTGCAAGGGGACCCAGGTGG AAAGACGGGGACTGAGGCAAGAGCAGCAGCAGCAGCAGCAGCAGCTGCCTGTGAACATACCTCAGACGCCT CGGCGGCCTGAGAACTTTAGGGTGACTGATGCTACCCCCACAGAGGGGCAAGAGCCCCCAGGACTAACAGCTGAC TGACCAAAGCAGCCCCTTGTAAGCAGCTCTGAGTCTTTTGGAGGACAGGGACGGTTTGTGGCTGAGATAAGTGTT AAAGGGTGGCCTTCTTGGGTAGCAGGAGTCAGGGGGGCTGTACCCTGGGGGTGCCAGGAAATGCTCTCTGACCTAT

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<subunit 1 of 1, 1184 aa, 1 stop</pre>

<MW: 129022, pI: 5.20, NX(S/T): 5

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Important features:

Signal peptide:

amino acids 1-13

Transmembrane domain:

amino acids 719-739

N-glycosylation site.

amino acids 415-418, 582-585, 659-662, 662-665 amd 857-860

Cadherins extracellular repeated domain signature.

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCAGTCCCGGCTGCAGCACCTGGGAGAAGG CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT CCCAGATACTATTTTTTGGATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGCACCAT GTTTGAGCTCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT GGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTCATGGTGCCTTTTTACATTGGC TATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTTCCTGTCTCTT ATGGCTGACCTTTATGTATTTCTTCTGGAAACTAGGAGATCCCTTTCCCCATTCTCAGCCCAA AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTTGGTGATTGGAGTGACTCTC ATGGCTCTTCTTCTGGATTTGGTGCTGTCAACTGCCCATACACTTACATGTCTTACTTCCT CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAA GTGCATAACAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGG TTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC AAGGGGAAATATTTTAATTTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAATTTT CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCACAAGAGGCA TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATT TCCTTCATTCTTGTTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCATTGTCCTGCTATTAGCAC AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGATCCGAATGAGTATGCCTTTAGAA TACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTT TGATGTGATCTTCCTGGTCAGCGCTCTCTCTAGCATACTCTTCCTCTATTTGGCTCACAAAC AGGCACCAGAGAAGCAAATGGCACCT**TGA**ACTTAAGCCTACTACAGACTGTTAGAGGCCAGT GGTTTCAAAATTTAGATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAAC AAACAAAATGCTATGGTAGCATTTTTCACCTTCATAGCATACTCCTTCCCCGTCAGGTGATA GCAGAGAGCATCCCGTGTGGATATGAGGCTGTGTAGAGGCGGAGAGGAGCCAAGAAACTAA AGGTGAAAAATACACTGGAACTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT AGGATTTCCGTTTTAAGGTTCACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT ACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI
LGVLNSSSRYFHWKMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFF
WKLGDPFPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ
QEVDALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF
DRVGKTDPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISS
SKSSNVIVLLLAQIMGMYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA
LSSILFLYLAHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398, 425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA
TCATGATTACCTCCCNGANACTATTTTTTGGATTTGGGTGGCTTTTCTTCNGCGCCAATGTT
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT
CTTGCACCATGTTTGAGCTCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT
TATTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCTTT
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTT
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC
TTTNTTGAATTCCGGGTTNNGNATACCTTCCCAGAAAATATTTTTTTGGATTTGGGTAGNTT
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT
NTCCGTGACGTTTGCATTTTCTTGCACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC
CTGGTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA
TAAACAACGACTGCTTTTTTCCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN
TAGGAGATCCCTTTCCCATTCTC

 $\tt CTCGCGCAGGGATCGTCCC{\color{blue}ATG}CCGGGGCTCGGAGCCGCGACCCTTGGGGGGCCTCCGGGATTTGCTACCTTTT$ TGGCTCCCTGCTCGAACTGCTCTTCTCACGGGCTGTCGCCTTCAATCTGGACGTGATGGGTGCCTTGCGCAA GGAGGCCAGCCAGCCTCTTCGGCTTCTCTGTGCCCTGCACCGGCAGTTGCAGCCCCGACCCCAGAGCTG GCTGCTGGTGGTGCTCCCCAGGCCCTGGCTCTTCCTGGGCAGCAGCGCGAATCGCACTGGAGGCCTCTTCGCTTG CCCGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAA GGAGAACCAGTGGTTGGGAGTCAGTGTTCGGAGCCAGGGGCCTGGGGGCAAGATTGTTACCTGTGCACACCGATA TGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATGATTGGTCGCTGCTTTGTGCTCAGCCAGGA ${\tt CCTGGCCATCCGGGATGAGTTGGATGGGGGAATGGAAGTTCTGTGAGGGACGCCCCCAAGGCCATGAACAATT}$ TGGGTTCTGCCAGCAGGGCACAGCTGCCGCCTTCTCCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAAC TCCCTACGAGGCGGGGGGAGAGAAGGAGCAGGACCCCCGCCTCATCCCGGTCCCTGCCAACAGCTACTTTGGCTT CTCTATTGACTCGGGGAAAGGTCTGGTGCGTGCAGAAGAGCTGAGCTTTGTGGCTGGAGCCCCCCGCGCCAACCA CAAGGGTGCTGTGGTCATCCTGCGCAAGGACAGCGCCAGTCGCCTGGTGCCCGAGGTTATGCTGTCTGGGGAGCG TGCCCCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTGCTGTGTATGTGTACTTGAACCAGGGGGGTCACTG GGCTGGGATCTCCCCTCTCCGGCTCTGCGGCTCCCCTGACTCCATGTTCGGGATCAGCCTGGCTGTCCTGGGGGA CCTCAACCAAGATGGCTTTCCAGATATTGCAGTGGGTGCCCCCTTTGATGGTGATGGGAAAGTCTTCATCTACCA TGGGAGCAGCCTGGGGGTTGTCGCCAAACCTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGG CGCAGTGCTCTTCAGGGCCAGACCCATCCTCCATGTCTCCCATGAGGTCTCTATTGCTCCACGAAGCATCGACCT GGAGCAGCCCAACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGGTCTGTTTCAGCTACATTGCAGTCCC CAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTGTTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGT TCCCCGTGTGACGTTCCTGAGCCGTAACCTGGAAGAACCCAAGCACCAGGCCTCGGGCACCGTGTGGCTGAAGCA CCAGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTCGGGCCATTGT AGTGACCTTGTCCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCCTGGCCAGGGGCTGCCTCCAGTGGC CCCCATCCTCAATGCCCACCCAGCCCAGCCGGGCAGAGATCCACTTCCTGAAGCAAGGCTGTGGTGAAGA ${\tt CAAGATCTGCCAGAGCAATCTGCAGCTGGTCCACGCCCGCTTCTGTACCCGGGTCAGCGACACGGAATTCCAACC}$ GGTCACCAACCTGCCATCGGACCCAGCCCCAGCCCCAGGCTGATGGGGATGATGCCCATGAAGCCCAGCTCCTGGT CATGCTTCCTGACTCACTGCACTACTCAGGGGTCCGGGCCCTGGACCCTGCGGAGAAGCCACTCTGCCTGTCCAA TGAGAATGCCTCCCATGTTGAGTGTGAGCTGGGGAACCCCATGAAGAGAGGTGCCCAGGTCACCTTCTACCTCAT CCTTAGCACCTCCGGGATCAGCATTGAGACCACGGAACTGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGAGCA GGAGCTGCATCCAGTCTCTGCACGAGCCCGTGTCTTCATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATTCC $\tt CCAGCAACTCTTCTTCTGGTGTGGGGGGGGGGGAGAGAGCCATGCAGTCTGAGCGGGATGTGGGCAGCAAGGT$ CAAGTATGAGGTCACGGTTTCCAACCAAGGCCAGTCGCTCAGAACCCTGGGCTCTGCCTTCCTCAACATCATGTG GCAGAAAGGGCTTTGCTCTCCCAGGCCCAACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGGCGGCGGGA GCTGGAGCCACCTGAGCAGGAGCCTGGTGAGCGGCAGGAGCCCAGCATGTCCTGGTGGCCAGTGTCCTCTGC TGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCACAGTGAAGTCCTCCATAAAGAACTTGATGCTCCGAGA TGCCTCCACAGTGATCCCAGTGATGGTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCCTGGTGGGT CAAACGGCGAAGCACCCGAGGCCACCGTGCCCCAGTACCATGCGGTGAAGATTCCTCGGGAAGACCGACAGCA GTTCAAGGAGAGAGACGGCCCCTGAGGAACACTGGGGCAGCCCCCGGCGGGAGGCCCCGGATGCACA TCCTCCCACCCAACTTCCCCTTAGAGTGCTGTGAGATGAGAGTGGGTAAATCAGGGACAGGGCCATGGGGTAGGG TGAGAAGGGCAGGGGTGTCCTGATGCAAAGGTGGGGAGAAGGGATCCTAATCCCTTCCTCTCCCATTCACCCTGT GTAACAGGACCCCAAGGACCTGCCTCCCCGGAAGTGCCTTAACCTAGAGGGTCGGGGAGGAGGTTGTGTCACTGA $\tt CTCAGGCTGCTCTCTAGTTTCCCCTCTCATCTGACCTTAGTTTGCTGCCATCAGTCTAGTGTTTCGTGGT$

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><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

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Important features:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT TGGATGATAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC AAATTCCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCCTTCGA TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC CCATGTCCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT GGAGTTCAGGGAAGTGGCAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAA GTCAAAACAAGAAGACAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTCGATACCAGCATC TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAACAGACTTGATACAAACTATGACCT GCTATTGGACCAGTCAGAGCTCAGAAGCATTTACCTTGATAAGAATGAACAGTGTACCAAGG CATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC CAACACAATGTCATGGCAGTGTTGGACAGTGCTGGTGTTGACAGATATGGAAATGAAGTC ATGGGATCCAGAATAAATGGTGTTGCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG CATGATGTATACATT**TGA**TTGATGACAGTTGAAATCAATAAATTCTACATTTCTAATATTTTA CAAAAATGATAGCCTATTTAAAATTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCA CATATATTTTGTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAACTTTATGTTTAAAT AAGAATCATTTGCTTTGAGTTTTTATATTCCTTACACAAAAAGAAAATACATATGCAGTCTA GTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTCACGAGAACAAACTTTGT AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAAG ATAATTCTAAGTGAAATTAAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG

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><MW: 49429, pI: 4.80, NX(S/T): 0

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Important features:

Signal peptide:

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

 ${\tt CAGACTCCAGATTTCCCTGTCAACCACGAGGAGTCCAGAGGAGGAAACGCGGAGCGAGACAACAGTACCTGACGC}$ GCTCTGCTCCGGTGCTGCCTGGGGCGGCCGGCTTCACACCTTCCCTCGATAGCGACTTCACCTTTACCCTT CCCGCCGCCAGAAGGAGTGCTTCTACCAGCCCATGCCCCTGAAGGCCTCGCTGGAGATCGAGTACCAAGTTTTA GATGGAGCAGGATTAGATATTGATTTCCATCTTGCCTCTCCAGAAGGCAAAACCTTAGTTTTTGAACAAAGAAAA TCAGATGGAGTTCACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAATACATTCAGCACCATT TCTGAGAAGGTGATTTCTTTGAATTAATCCTGGATAATATGGGAGAACAGGCACAAGAACAAGAATTGGAAG AAATATTACTGGCACAGATATATTGGATATGAAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCC AGACTAAGCAAAAGTGGGCACATACAAATTCTGCTTAGAGCATTTGAAGCTCGTGATCGAAACATACAAGAAAGC AACTTTGATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTCATGGTGGTGGTGTCAGCCATTCAAGTTTAT ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAACTT**AA**AACTCCAAACTAGAGTACGTAACATTGAAA AATGAGGCATAAAAATGCAATAAACTGTTACAGTCAAGACCATTAATGGTCTTCTCCAAAATATTTTGAGATATA AAAGTAGGAAACAGGTATAATTTTAATGTGAAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAG AGTCTGTTTTTAACAGGTTCTATTACCCAGAACTTTTTTGTAAATGCGGCAGTTACAAATTAACTGTGGAAGTTT TCAGTTTTAAGTTATAAATCACCTGAGAATTACCTAATGATGGATTGAATAAATCTTTAGACTACAAAAGCCCAA CTTTTCTCTATTTACATATGCATCTCTCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTG AGATTTTTATAACCAAATACATTTCAGTGTAACATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTC ${\tt CCAAAAGCTGACATTTTCACGATTCTTAAAAACACAAAGTTACACTTACTAAAATTAGGACATGTTTTCTCTTTG}$ AAATGAAGAATATAGTTTAAAAGCTTCCTCCTCCATAGGGACACATTTTCTCTAACCCTTAACTAAAGTGTAGGA TTTTAAAATTAAATGTGAGGTAAAATAAGTTTATTTTTAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA TAATCATGTTATGTTAATTTTTAACATGATTGCTGACTTGGATAATTCATTATTACCAGCAGTTATGAAGGAAATA TTGCTAAAATGATCTGGGCCTACCATAAATAAATATCTCCTTTTCTGAGCTCTAAGAATTATCAGAAAAACAGGAA AAACTTTGGCTGTAGGTTTTTATTTTCTACAAGAATTCTGGTTTGAATTATTTTTTGTAAGCAGGTACATTTTATA TAAAATGGCCTTTCTGAACACTTTATTTATTGATGTTGAAGTAAGGATTAGAAACATAGACTCCCAAGTTTTAAA CACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTTGAAGTCTATGGGGGTCTTAC TCAAGTACTAGTAATTTAACTTCATCATGAATGAACTATAATTTTTAAGTTATGCCCATTTATAACGTTGTTTAT GACTACATTGTGAGTTAGAAACAAACTTAAAATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATT CTTGATGAGCAATAATGATAACCAGAGAGTGATTTCATTTACACTCATAGTAGTATAAAAAGAGATACATTTCCC TCTTAGGCCCCTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAAAATGAGGTAAATGCCGTAT ATGATCAATTACCTTAATTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCCTCTGCAACACTTGCAGAACAA AGGTCAATAAGATCCTTGCCTATGAATACCCCTCCCTTTTGCGCTGTTAAATTTGCAATGAGAAGCAAATTTACA GTACCATAACTAATAAAGCAGGGTACAGATATAAACTACTGCATCTTTTCTATAAAACTGTGATTAAGAATTCTA CCTCTCCTGTATGGCTGTTACTGTACTGTACTCTGACTCCTTACCTAACAATGAATTTGTTACATAATCTTCT ACATGTATGATTTGTGCCACTGATCTTAAACCTATGATTCAGTAACTTCTTACCATATAAAAACGATAATTGCTT TATTTGGAAAAGAATTTAGGAATACTAAGGACAATTATTTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG CATAACCAAAAAAGCAAAACTTGTAAACAGAGTAAAAATCTTTAATATTTCTAAAGACATACTGTTTATCTGCTT CATATGCTTTTTTTAATTTCACTATTCCATTTCTAAATTAAAGTTATGCTAAATTGAGTAAGCTGTTTATCACTT AACAGCTCATTTTGTCTTTTTCAATATACAAATTTTAAAAAATACTACAATATTTAACCTAAGGCCCAACCGATTTC CATAATGTAGCAGTTACCGTGTTCACCTCACACTAAGGCCTAGAGTTTGCTCTGATATGCATTTGGATGATTAAT $\tt GTTATGCTGTTCTTTCATGTGAATGTCAAGACATGGAGGGTGTTTGTAATTTTATGGTAAAATTAATCCTTCTTA$ CACATAATGGTGTCTTAAAATTGACAAAAAATGAGCACTTACAATTGTATGTCTCCTCAAATGAAGATTCTTTAT GTGAAATTTTAAAAGACATTGATTCCGCATGTAAGGATTTTTCATCTGAAGTACAATAATGCACAATCAGTGTTG $\tt CTCAAACTGCTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATAATAA$ AAATTATCAAAGGAAAA

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196</pre>

><subunit 1 of 1, 229 aa, 1 stop

><MW: 26017, pI: 4.73, NX(S/T): 0

MGDKIWLPFPVLLLAALPPVLLPGAAGFTPSLDSDFTFTLPAGQKECFYQPMPLKASLEIEY QVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCFDNTFSTISEKVIFFEL ILDNMGEQAQEQEDWKKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN IQESNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965</pre>

<subunit 1 of 1, 175 aa, 1 stop</pre>

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405</pre>

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP FQGDSTVTKSCASKCKPSDVDGIGQTLPVSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL

Important features:

Signal peptide:

amino acids 1-17

N-glycosylation site.

amino acids 46-49

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC GAGTCCTTCTGAG**ATG**ATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTCGCGATGG TAGCGGCGGCTCTCGGCGGCCACCTCTGCTGGGAGTGAGCGCCACCTTGAACTCGGTTCTC AATTCCAACGCTATCAAGAACCTGCCCCCACCGCTGGGCGCGCTGCGGGGCACCCAGGCTC TGCAGTCAGCGCCGCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGCCACTGATGAGTACTGCGCTAGT CCCACCGCGGGGGGGCGCGCGCGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA GACACTTCTGGTCCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCAT AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTCAGA GACACTAAACCAGCTATCCAAATGCAGTGAACTCCTTTTATATAATAGATGCTATGAAAACC TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT TCCAATAACACCTTCCAAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACTCCCCTG TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA AACTTTTAATTATTTTCTAAAGGTGCTGCACTGCCTATTTTTCCTCTTGTTATGTAAATTT TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT TCAGCTTATAGTTCTTAAAAGCATAACCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA AGGATCTCTTGGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA AATAAAATTTAACATTTAAAAAAAAAAAAA

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530</pre>

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA
APGILYPGGNKYQTIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRRKRCMRH
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQ
KDHHQASNSSRLHTCQRH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

GAGGAACCTACCGGTACCGGCCGCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATCCCGTGCGCCGCG $\tt GGGTTTGAGGATGGGGGGGGTAGCTACAGGAAGCGACCCCGCGATGGCAAGGTATATTTTTGTGGAATGAAAAGGA$ AGTATTAGAAATGAGCTGAAGACCATTCACAGATTAATATTTTTTGGGGACAGATTTGTGATGCTTGATTCACCCT TGAAGTAATGTAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTTCAC GATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTTACAGTTTACTTGG AGTGTCCAAAACTGCAAGCAGTAGAGAAATAAGACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCCTGATAA TCTACGGAAAAAGTATGACAAATATGGAGAAAAGGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA CTATTATCGTTATGATTTTTGGTATTTATGATGATCCTGAAATCATAACATTGGAAAGAAGAAGAATTTGATGC CACATGGAGAGCTTTGCTAAAGAAGTGGATGGGTTACTTCGAATTGGAGCTGTTAACTGTGGTGATGATAGAAT $\tt GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCCAGTCTCTTCATTTTTCGGTCTGGAATGGCCCCAGTGAAATA$ TCATGGAGACAGATCAAAGGAGAGTTTAGTGAGTTTTGCAATGCAGCATGTTAGAAGTACAGTGACAGAACTTTG GACAGGAAATTTTGTCAACTCCATACAAACTGCTTTTGCTGCTGGTATTGGCTGGTGATCACTTTTTGTTCAAA AGGAGGAGATTGTTTGACTTCACAGACACGACTCAGGCTTAGTGGCATGTTGTTTCTCAACTCATTGGATGCTAA AGAAATATATTTGGAAGTAATACATAATCTTCCAGATTTTGAACTACTTTCGGCAAACACACTAGAGGATCGTTT AAAAACTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGACTGTTCCTCTGCACCAGACATCTGTAGTAA TCTGTATGTTTTTCAGCCGTCTCTAGCAGTATTTAAAGGACAAGGAACCAAAGAATATGAAATTCATCATGGAAA GAAGATTCTATATGATATACTTGCCTTTGCCAAAGAAAGTGTGAATTCTCATGTTACCACGCTTGGACCTCAAAA ${\tt TTTTCCTGCCAATGACAAGAACCATGGCTTGTTGATTTCTTTGCCCCCTGGTGTCCACCATGTCGAGCTTTACT}$ ACCAGAGTTACGAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTCATGA GGGACTCTGTAACATGTATAACATTCAGGCTTATCCAACAACAGTGGTATTCAACCAGTCCAACATTCATGAGTA ACCCACCATCAACGAACTAGTTACACAAAGAAAACACAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTG GTGTCATCCTTGCCAAGTCTTAATGCCAGAATGGAAAAGAATGGCCCGGACATTAACTGGACTGATCAACGTGGG CAGTATAGATTGCCAACAGTATCATTCTTTTTGTGCCCAGGAAAACGTTCAAAGATACCCTGAGATAAGATTTTT TCCCCCAAAATCAAATAAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGATGCTTATTCCCTGAGAAT CTGGGGTCTAGGATTTTTACCTCAAGTATCCACAGATCTAACACCTCAGACTTTCAGTGAAAAAAGTTCTACAAGG GAAAAATCATTGGGTGATTGATTTCTATGCTCCTTGGTGTGGACCTTGCCAGAATTTTGCTCCAGAATTTGAGCT CTTGGCTAGGATGATTAAAGGAAAAGTGAAAGCTGGAAAAGTAGACTGTCAGGCTTATGCTCAGACATGCCAGAA AGCTGGGATCAGGGCCTATCCAACTGTTAAGTTTTATTTCTACGAAAGAGCAAAGAGAAATTTTCAAGAAGAGCA GATAAATACCAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAAAAATTGGAAACTCTCCGAAATCAAGGCAA GAGGAATAAGGATGAACTT<u>TGA</u>TAATGTTGAAGATGAAGAAAAAGTTTAAAAGAAATTCTGACAGATGACATCAG GAATTATCTACAGCACTGGTGTAAAAGAAGGGTCTGCAAACTTTTTCTGTAAAGGGCCGGTTTATAAATATTTTA GACTTTGCAGGCTATAATATATGGTTCACACATGAGAACAAGAATAGAGTCATCATGTATTCTTTGTTATTTGCT TTTAACAACCTTTAAAAAATATTAAAACGATTCTTAGCTCAGAGCCATACAAAAGTAGGCTGGATTCAGTCCATG ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTCACGTTTTTTGGCTGACCTGAAAAGAGGTAACT TAGTTTTTGGTCACTTGTTCTCCTAAAAATGCTATCCCTAACCATATATTTATATTTTCGTTTTAAAAACACCCAT TAGCAATTAACTGGGCATTGTAGAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATA TGTGTTCATGTATTTTCTGAAATTGCTTTCATAGAAATTTTCCCACTGATAGTTGATTTTTGAGGCATCTAATAT TTTTTCACTCCTGTCCAGTCTATTTATTATTCAAATAGGAAAAATTACTTTACAGGTTGTTTTACTGTAGCTTAT AATGATACTGTAGTTATTCCAGTTACTAGTTTACTGTCAGAGGGCTGCCTTTTTCAGATAAATATTGACATAATA ${\tt ACTGAAGTTATTTTATAAGAAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTTTAGA}$ CTCAAAGAATCACAAATTTGTCAGTAACATGTAGTTGTTTAGTTATAATTCAGAGTGTACAGAATGGTAAAAATT

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439</pre>

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKL
HPDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKGLEDNQGGQYESWNYYRYDFGI
YDDDPEIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC
GDDRMLCRMKGVNSYPSLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNS
IQTAFAAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN
TLEDRLAHHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQP
SLAVFKGQGTKEYEIHHGKKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFFAPWC
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIHEYEGHHS
AEQILEFIEDLMNPSVVSLTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG
FLPQVSTDLTPQTFSEKVLQGKNHWVIDFYAPWCGPCQNFAPEFELLARMIKGKVKAGKVDC
QAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAIAALISEKLETLRNQGKRNKDEL

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGA GTCGTTGGTGAAGTTTTTCATTCCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAAACTGCAGCTGAGTGCCGAAA ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT CTCTAAATCAGGTGAAGAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA CATCCTAGGACATTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCCTTACCTCATCCCATAT TGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTCAGGCCTT GGGAAAAACTGGTATCAAAACCTCATGTCTCTGCCCAGTTTTTGTGAATACTGGGTTCACCA AAAATCCAAGCACAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA GATGGAATACTTACCAATAAGAAAATGATTTTTGTTCCATCGTATATCAATATCTTTCTGAG ACTACAGAAGTTTCTTCCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT TATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAGCTTTATTTCACATTTTT TCAGTCCTGATAATATTAAAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA ATTACCTGTCTTCCTGTTTCTCAAGAATATTTACGTAGTTTTTCATAGGTCTGTTTTTCCTT TCATGCCTCTTAAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT TTTATTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAACT TATTTACACAGGGAAGGTTTAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG ATCTCAACCTGGACATATTTTAAGATTCAGCATTTGAAAGATTTCCCTAGCCTCTTCCTTTT TCATTAGCCCAAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT AACTCTGAAGTCCACCAAAAGTGGACCCTCTATATTTCCTCCCTTTTTATAGTCTTATAAGA TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAGTTCTAGCCCCATGA TAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGATGTTTAGACAAT TTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAACTGTACTGGCTATTACATAAGAAA CAATGGACCCAAGAGAAGAA

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409</pre>

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI LVLWDINKRGVEETAAECRKLGVTAHAYVVDCSNREEIYRSLNQVKKEVGDVTIVVNNAGTV YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFVNTGFTKNPSTRLWPVLETDEVVRSLID GILTNKKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site. amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein amino acids 165-202, 37-49, 112-122 and 210-219

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGCGCGAGGTTCCCAGCAGG AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTCATGATCCT GCTGATCATCGTGTACTGGGACAGCGCAGGCGCGCGCACTTCTACTTGCACACGTCCTTCT CTAGGCCGCACACGGGGCCGCCGCTGCCCACGCCCGGGCCGGACAGGGACAGGGAGCTCACG GCCGACTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA CCTTCCCAGAAAGGAGACGGAGCAGCCGCCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACTCCAGCCTGGCCTTCCCCACCAAGGAGCG CGCATTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGG CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA CGTGCACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT $\tt CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCCTCTTCGTGCGCGACCCC$ TTCGTGCGCCTGATCTCCGCCTTCCGCAGCAGCTTCGAGCTGGAGAACGAGGAGTTCTACCG CAAGTTCGCCGTGCCCATGCTGCGGCTGTACGCCAACCACCAGCCTGCCCGCCTCGGCGC GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGAC CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCCGAGCTACCGGAACAGG ${\tt ACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT}$ GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC ATTGAGTACTGTATCGATATTGTTTTTTAAGATTAATATTTCAGGTATTTAATACGA

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112</pre>

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGSVFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRELTA
DSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAER
RSVLRGFCANSSLAFPTKERAFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLS
GSLLHRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF
VRLISAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDP
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLDEDAAQLLQLLQVDRQLRFPPSYRNRT
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

Important features:

Signal peptide:

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein amino acids 329-332

TCGGGCCAGAATTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA ${\tt AAGAGGCCCAGAGTAGAGAGAGAGAGAGACCGACGTACACGGG} \underline{{\tt ATG}} {\tt GCTACGGGAACGCGCT}$ ATGCCGGGAAGGTGGTCGTGACCGGGGGCGGGCGCGCATCGGAGCTGGGATCGTGCGC GCCTTCGTGAACAGCGGGGCCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCCGGC CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG ${\tt TGAAGACCCTGGTTTCTGAGACCATCCGCCGATTTGGCCGCCTGGATTGTGTTGTCAACAAC}$ GCTGGCCACCACCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCCTACCTGCGGA AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCCAATCGGCCAGGCCCAGGCA GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCCAG $\tt CCACTGGGCCGCATGGGCCAGCCCGCTGAGGTCGGGGCTGCGGCAGTGTTCCTGGCCTCCGA$ AGCCAACTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGGTGCAGAGCTGGGGTACGGGT $\texttt{GCAAGGCCAGTCGGAGCACCCCGTGGACGCCCCCGATATCCCTTCC} \underline{\textbf{TGA}} \texttt{TTTCTCTCATTT}$ $\tt CTACTTGGGGCCCCCTTCCTAGGACTCTCCCACCCCAAACTCCAACCTGTATCAGATGCAGC$ $\tt CCCCAAGCCCTTAGACTCTAAGCCCAGTTAGCAAGGTGCCGGGTCACCCTGCAGGTTCCCAT$ AAAAACGATTTGCAGCC

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045</pre>

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVTGGGRGIGAGIVRAFVNSGARVVICDKDESGGRALEQELPGAVFILCD VTQEDDVKTLVSETIRRFGRLDCVVNNAGHHPPPQRPEETSAQGFRQLLELNLLGTYTLTKL ALPYLRKSQGNVINISSLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTGG AELGYGCKASRSTPVDAPDIPS

Important features:

N-glycosylation site.

amino acids 138-141

Short-chain alcohol dehydrogenase family protein amino acids 10-22, 81-91, 134-171 and 176-185

AGGCGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGCGGAATGGACCTGGCCTCACAACCTG
CTGTTTCTTCTTACCATTTCCATCTTCCTGGGGCTGGCCCAGCCCAGGAGCCCCAAAAGCAA
GAGGAAGGGGCAAGGGCGGCCTGGGCCCCTGGCCCCTCACCAGGTGCCACTGGACC
TGGTGTCACGGATGAAACCGTATGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG
GTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCT
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCC
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTTCTGGGCTGTGTAACCCCTTCACC
ATGCAGGAGGACCGCCAGCACAGGGCCTTGCCGGCCAGCGCCAGCTCATCAGCACCCCTTCACC
CCTCTGCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCAGCCCAGCCCCGAGA
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GCAAG

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<subunit 1 of 1, 180 aa, 1 stop
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ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPSRIPVDLPEARCLCL
GCVNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF</pre>

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

GCGCCGCCAGGCGTAGGCGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGG GCGCCCAACATGGCGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCCTGGAT CGCGGCTGTGGCGGCGACGCCCCGAGGAGGCCGCGCTGCCGCCGGAGCAGAGCCGGG TCCAGCCCATGACCGCCTCCAACTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT TACGCCCCATGGTGTCCATCCTGCCAGCAGACTGATTCAGAATGGGAGGCTTTTGCAAAGAA TGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTG GCCGCTTCTTTGTCACCACTCTCCCAGCATTTTTTCATGCAAAGGATGGGATATTCCGCCGT TATCGTGGCCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACTATTTCACAGTGACTCTTGGAATT CCTGCTTGGTGTTCTTATGTGTTTTTCGTCATAGCCACCTTGGTTTTTTGGCCTTTTTATGGG TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG GAGGAAAAAGATGATTCAAATGAAGAAGAAAACAAAGACAGCCTTGTAGATGATGAAGAAGA GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGAGGAGGACGACTTGGCTG CTGGTGTGGATGAGGAGAGAGTGAGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTG ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCCAGC TGACACAGAGGTGGTAGAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGAC TGTAGATTTAATGATGCGTTTTCAAGAATACACACCAAAACAATATGTCAGCTTCCCTTTGG CCTGCAGTTTGTACCAAATCCTTAATTTTTCCTGAATGAGCAAGCTTCTCTTAAAAGATGCT CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT GACAATCAGGATATAGAAAAACAAACGTAGTGTTGGGATCTGTTTGGAGACTGGGATGGGAA CAAGTTCATTTACTTAGGGGTCAGAGAGTCTCGACCAGAGGGGGCCATTCCCAGTCCTAATC AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCT CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGCATCCTTTTCTTGTGTAAAGTATTTAT TTTTGTCAAATTGCAGGAAACATCAGGCACCACAGTGCATGAAAAATCTTTCACAGCTAGAA ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTG TGCTATGTTTTATTTCTTACCTTTAATTTTTCCAGCATTTCCACCATGGGCATTCAGGCTCT CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC TGTGTTTGTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTGT GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAAGGAAGTAAGGATT AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCCTCTAAGTCTTGCCAGTACAAGGTAGT CTTGTGAAGAAAGTTGAATACTGTTTTGTTTTCATCTCAAGGGGTTCCCTGGGTCTTGAAC TACTTTAATAATAACTAAAAAACCACTTCTGATTTTCCTTCAGTGATGTGCTTTTGGTGAAA GAATTAATGAACTCCAGTACCTGAAAGTGAAAGATTTGATTTTGTTTCCATCTTCTGTAATC TTCCAAAGAATTATATCTTTGTAAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG GCTAATTTCTTT

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<subunit 1 of 1, 349 aa, 1 stop

<MW: 38952, pI: 4.34, NX(S/T): 1

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Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide isomerase) amino acids 56-72

Flavodoxin proteins

amino acids 173-187

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAAACTCCGGTAAGTACCTAGCCCACATGATT CAAATGCTATATCTATTCAGGGGCTCTCAAGAACA**ATG**GAATATCATCCTGATTTAGAAAAT TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCTGTAATTTTGG GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGGTTCTTTCC AGCCCTTGTCCTCCTAATTGGATTATATGAGAAGAGCTGTTATCTATTCAGCATGTCACT AAATTCCTGGGATGGAAGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG ACAGCTCAAATGAATTGGGATTTATAGTAAAACAAGTGTCTTCCCAACCTGATAATTCATTT CTCTTCTAACTTATTTCAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCAAATTGTG TATGGATTCACGTGTCAGTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT AGGAGGACAGAAAACAGAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATG TTTAGAGAGCTTGGCCAACTGTAATCTTAACCAAGAAATTGAAGGGAGAGGCTGTGATTTCT CACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC CTCAGCCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTGGTG TTTTTTGTAGAGACTGGGTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAG TGATCTGCCCGCCTTGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCACACCTGGC CCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTTACCTTGGGTAAGCCATAAGCGA ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGGT GTGTTGCCACGATTTGACCCTCAACTTCTAGCAGTATATCAGTTATGAACTGAGGGTGAAAT ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAAATCTTCACCACAGTCAGAGCAATTTT ATTATTTTCATCAGTATGATCATAATTATGATTATCATCTTAGTAAAAAGCAGGAACTCCTA CTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT TTTTTTTTTTTTTTTTGAGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTGCAACGG CACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCT CCCAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTTTAGT AGAGACAGGGTTTCTCCATGTCGGTCAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGC CTGCCTCGGCCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCAGCCTAGAATCT TGTATAATATGTAATTGTAGGGAAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTAAATACA ACAAGTATTAACATTTTGGAATATGTTTTATTAGTTTTTGTGATGTACTGTTTTACAATTTTT ACCATTTTTTTCAGTAATTACTGTAAAATGGTATTATTGGAATGAAACTATATTTCCTCATG TGCTGATTTGTCTTATTTTTTCATACTTTCCCACTGGTGCTATTTTTATTTCCAATGGATA TTTCTGTATTACTAGGGAGGCATTTACAGTCCTCTAATGTTGATTAATATGTGAAAAGAAAT TGTACCAATTTTACTAAATTATGCAGTTTAAAATGGATGATTTTATGTTATGTTGGATTTCAT

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<MW: 22563, pI: 4.87, NX(S/T): 1

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Important features:

Type II transmembrane domain:

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site. amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

GGAAGGGGAGGAGCAGGCCACACAGGCACGGCCGGTGAGGGACCTGCCCAGACCTGGAGGGTCTCGCTCTGTCA CACAGGCTGGAGTGCAGTGTGTCTTGGCTCATCGTAACCTCCACCTCCCGGGTTCAAGTGATTCTCATGCC TCAGCCTCCGAGTAGCTGGGATTACAGGTGGTGACTTCCAAGAGTGACTCCGTCGGAGGAAA**ATG**ACTCCCCAG TCGCTGCTGCAGACGACACTGTTCCTGCTGAGTCTGCTCTTCCTGGTCCAAGGTGCCCACGGCAGGGGCCACAGG GAAGACTTTCGCTTCTGCAGCCAGCGGAACCAGACACAGAGCAGCCTCCACTACAAACCCACACCAGACCTG CGCATCTCCATCGAGAACTCCGAAGAGGCCCTCACAGTCCATGCCCCTTTCCCTGCAGCCCACCCTGCTTCCCGA TCCTTCCCTGACCCCAGGGGCCTCTACCACTTCTGCCTCTACTGGAACCGACATGCTGGAGATTACATCTTCTC TATGGCAAGCGTGACTTCTTGCTGAGTGACAAAGCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGGAGAGCCTG GCTCAGGGCCCCCGCTGTTAGCCACTTCTGTCACCTCCTGGTGGAGCCCTCAGAACATCAGCCTGCCCAGTGCC GCCAGCTTCACCTTCCACAGTCCTCCCCACACGCCGCTCACAATGCCTCGGTGGACATGTGCGAGCTC AAAAGGGACCTCCAGCTGCTCAGCCAGTTCCTGAAGCATCCCCAGAAGGCCTCAAGGAGGCCCTCGGCTGCCCCC GCCAGCCAGCAGTTGCAGAGCCTGGAGTCGAAACTGACCTCTGTGAGATTCATGGGGGACATGGTGTCCTTCGAG GAGGACCGGATCAACGCCACGGTGTGGAAGCTCCAGCCCACAGCCGGCCTCCAGGACCTGCACATCCACTCCCGG CAGGAGGAGGAGCAGAGCCAGATCATGGAGTACTCGGTGCTGCTGCTCGAACACTCTTCCAGAGGACGAAAGGC CGGAGCGGGGAGCTGAGAAGAGACTCCTCCTGGTGGACTTCAGCAGCCCAGCCCTGTTCCAGGACAAGAATTCC AGCCAAGTCCTGGGTGAGAAGGTCTTGGGGATTGTGGTACAGAACACCAAAGTAGCCAACCTCACGGAGCCCGTG GTGCTCACTTTCCAGCACCAGCTACAGCCGAAGAATGTGACTCTGCAATGTGTGTTCTGGGTTGAAGACCCCACA TTGAGCAGCCCGGGGCATTGGAGCAGTGCTGGGTGTGAGACCGTCAGGAGAGAAACCCAAACATCCTGCTTCTGC AACCACTTGACCTACTTTGCAGTGCTGATGGTCTCCTCGGTGGAGGTGGACGCCGTGCACAAGCACTACCTGAGC GTGCCCTGCCGTGCAGGAGGAAACCTCGGGACTACACCATCAAGGTGCACATGAACCTGCTGCTGCTGCTCTTC ATCTTCCTGCACTTCTCCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGGTACAACCTCTACCGACTCGTG GTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTT CTGGTGACGCTGGTGGCCCTGGTGGATGTGGACAACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAG GGCGTCATCTACCCTTCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGC CTGGTGTTTCTGTTCAACATGGCCATGCTAGCCACCATGGTGGTGCAGATCCTGCGGCTGCGCCCCCACACCCAA AAGTGGTCACATGTGCTGACACTGCTGGGCCTCAGCCTGGTCCTTGGCCTGGGCCTTGATCTTCTTCTCCC TTCATCTGGTACTGGTCCATGCGGCTGCAGGCCCGGGGTGGCCCCTCCCCTCTGAAGAGCAACTCAGACAGCGCC CAGAGATGCGGCCTCGTCGCACACTGCCTGTGGCCCCCGAGCCAGGCCCAGGCCCAGGCCAGTCAGCCGCAGACT GCCTTGGGGACTACTCGGCTCTCACTCAGCTCCCACGGGACTCAGAAGTGCGCCGCCATGCTGCCTAGGGTACTG TCCCCACATCTGTCCCAACCCAGCTGGAGGCCTGGTCTCTCCTTACAACCCCTGGGCCCAGCCCTCATTGCTGGG GTTGCTCTGTCTCTCGTGGTCACCCTGAGGGCACTCTGCATCCTCTGTCATTTTAACCTCAGGTGGCACCCAGGG CGAATGGGGCCCAGGGCAGACCTTCAGGGCCAGAGCCCTGGCGGAGGAGAGGCCCTTTGCCAGGAGCACAGCAGC ${\tt TCCTCTCCCAGGGCCTCCTTGCTCCTTCGTTCACAGCTGGGGGTCCCCGATTCCAATGCTGTTTTTTGGGGA}$ GTGGTTTCCAGGAGCTGCCTGGTGTCTGCTGTAAATGTTTGTCTACTGCACAAGCCTCGGCCTGCCCCTGAGCCA GGCTCGGTACCGATGCGTGGGCTGGGCTAGGTCCCTCTGTCCATCTGGGCCTTTGTATGAGCTGCATTGCCCTTG $\tt CTCACCCTGACCAAGCACGCCTCAGAGGGGCCCTCAGCCTCTCTGAAGCCCTCTTGTGGCAAGAACTGTGGA$ $\verb|CCATGCCAGTCCCGTCTGGTTTCCATCCCACCACTCCAAGGACTGAGACTGACCTCCTCTGGTGACACTGGCCTA|\\$ GAGCCTGACACTCTCCTAAGAGGTTCTCCCAAGCCCCCAAATAGCTCCAGGCGCCCCTCGGCCGCCCATCATGGT GGGAGCCATCATTCCTGCCTGGGAATCCTGGAAGACTTCCTGCAGGAGTCAGCGTTCAATCTTGACCTTGAAGAT GGGAAGGATGTTCTTTTACGTACCAATTCTTTTGTCTTTTGATATTAAAAAGAAGTACATGTTCATTGTAGAGA

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<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

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QEESLAQGPPLLATSVTSWWSPQNISLPSAASFTFSFHSPPHTAAHNASVDMCELKRDLQLL
SQFLKHPQKASRRPSAAPASQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD
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TQTSCFCNHLTYFAVLMVSSVEVDAVHKHYLSLLSYVGCVVSALACLVTIAAYLCSRVPLPC
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ISSGSTSSSRI

Important features:

Signal peptide:

amino acids 1-25

Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590 and 634-657

Microbodies C-terminal targeting signal.

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327 and 341-344

G-protein coupled receptors family 2 proteins

amino acids 475-504

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA
GGAAANCNTCGGGACTACACCNTCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCCTGCTG
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GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGG
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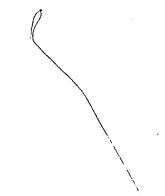
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Signal sequence:

amino acids 1-14

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATTCCATTTTGGAAGA AGACTAAAAATGGTGTTTCCAATGTGGACACTGAAGAGACAAATTCTTATCCTTTTTAACATAATCCTAATTTCC AAACTCCTTGGGGCTAGATGGTTTCCTAAAACTCTGCCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTG ATCGTGGACTGCACAGACAAGCATTTGACAGAAATTCCTGGAGGTATTCCCACGAACACCACGAACCTCACCCTC ACCATTAACCACATACCAGACATCTCCCCAGCGTCCTTTCACAGACTGGACCATCTGGTAGAGATCGATTTCAGA TGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCAGATTAAACCCAGAAGC CCTAGCTTACAGCTTCTCAGCCTTGAGGCCAACAACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCC AACATAGAAATACTCTACCTGGGCCAAAACTGTTATTATCGAAATCCTTGTTATGTTTCATATTCAATAGAGAAA GATGCCTTCCTAAACTTGACAAAGTTAAAAGTGCTCTCCCTGAAAGATAACAATGTCACAGCCGTCCCTACTGTT TTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAAATCCAAGAAGATGATTTAATAAC CTCAACCAATTACAAATTCTTGACCTAAGTGGAAATTGCCCTCGTTGTTATAATGCCCCATTTCCTTGTGCGCCC TGTAAAAATAATTCTCCCCTACAGATCCCTGTAAATGCTTTTGATGCGCTGACAGAATTAAAAGTTTTACGTCTA ${\tt CAAAACTTCTTGGCCAAAGAAATTGGGGGATGCTAAATTTCTGCATTTTCTCCCCAGCCTCATCCAATTGGATCTG}$ TCTTTCAATTTTGAACTTCAGGTCTATCGTGCATCTATGAATCTATCACAAGCATTTTCTTCACTGAAAAGCCTG AAAATTCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGAAAAGCTTTAACCTCTCGCCATTACATAATCTTCAA AATCTTGAAGTTCTTGGTCTTGGCACTAACTTTATAAAAATTGCTAACCTCAGCATGTTTAAACAATTTAAAAAGA CTGAAAGTCATAGATCTTTCAGTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAAT GCCAGAACTTCTGTAGAAAGTTATGAACCCCAGGTCCTGGAACAATTACATTATTTCAGATATGATAAGTATGCA ${\tt AGGAGTTGCAGATTCAAAAACAAAGAGGCTTCTTTCATGTCTGTTAATGAAAGCTGCTACAAGTATGGGCAGACC}$ AATCTGTCAGGAAATCTCATTAGCCAAACTCTTAATGGCAGTGAATTCCAACCTTTAGCAGAGCTGAGATATTTG GACTTCTCCAACAACCGGCTTGATTTACTCCATTCAACAGCATTTGAAGAGCTTCACAAACTGGAAGTTCTGGAT ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAAACTTTACCAAGAACCTAAAGGTT ACTCTGGAATTCAGAGGAAATCACTTAGATGTTTTATGGAGAGAGGTGATAACAGATACTTACAATTATTCAAG ${\tt AATCTGCTAAAATTAGAGGAATTAGACATCTCTAAAAATTCCCTAAGTTTCTTGCCTTCTGGAGTTTTTGATGGT}$ ATGCCTCCAAATCTAAAGAATCTCTCTTTGGCCAAAAATGGGCTCAAATCTTTCAGTTGGAAGAAACTCCAGTGT AGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAGTCTGACGAAGTATTTTCTACAAGATGCCTTC CAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAAGACCAGCTTCCCAGAAAATGTCCTC GTTAACCATACGGAGGTGACTATTCCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGGGCACACAAGGGC CAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA ${\tt TCTGTATCTCTCTTTTCTCATGGTGATGATGACAGCAAGTCACCTCTATTTCTGGGATGTGTGTATATTTACCAT}$ TTCTGTAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTAT CAGCTTAGCAAAAAGACAGTGTTTGTGATGACAGACAAGTATGCAAAGACTGAAAATTTTAAGATAGCATTTTAC TTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTCAGAAG CCATACTTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGAA ${\tt ACGGTCTAGCCCTTCTTTGCAAAACACAACTGCCTAGTTTACCAAGGAGAGGCCTGGC}$



MVFPMWTLKROILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGG IPTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRCNCVPIPLGSKNNMCIKRLQIKPRSFS GLTYLKSLYLDGNOLLEIPOGLPPSLOLLSLEANNIFSIRKENLTELANIEILYLGQNCYYR NPCYVSYSIEKDAFLNLTKLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNL NQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWF KNINKLOELDLSONFLAKEIGDAKFLHFLPSLIOLDLSFNFELOVYRASMNLSQAFSSLKSL KILRIRGYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQ TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH STAFEELHKLEVLDISSNSHYFOSEGITHMLNFTKNLKVLOKLMMNDNDISSSTSRTMESES LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSL AKNGLKSFSWKKLOCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQ DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDAVWFVWWVNHTEVTIP YLATDVTCVGPGAHKGOSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDVW YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPAVTEWVLAELVAKLEDPREKHFNLCLEE RDWLPGOPVLENLSOSIOLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVIILIFLE KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHPYFWQCLKNALATDNHVAYSQVFKETV

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 840-860

 ${\tt GGGTACCATTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGAACAACAGAAAC\underline{{\tt ATG}}{\tt GAAAACATGTTCCTTC}$ AGTCGTCAATGCTGACCTGCATTTTCCTGCTAATATCTGGTTCCTGTGAGTTATGCGCCGAAGAAAATTTTTCTA GAAGCTATCCTTGTGATGAGAAAAAGCAAAATGACTCAGTTATTGCAGAGTGCAGCAATCGTCGACTACAGGAAG CATTTCAAGGGCTGCAAAATCTCACTAAAATAAATCTAAACCACAACCCCAATGTACAGCACCAGAACGGAAATC CCGGTATACAATCAAATGGCTTGAATATCACAGACGGGGCATTCCTCAACCTAAAAAACCTAAGGGAGTTACTGC TTGAAGACAACCAGTTACCCCAAATACCCTCTGGTTTGCCAGAGTCTTTGACAGAACTTAGTCTAATTCAAAACA ATATATACAACATAACTAAAGAGGGCATTTCAAGACTTATAAACTTGAAAAATCTCTATTTGGCCTGGAACTGCT ATTTTAACAAAGTTTGCGAGAAAACTAACATAGAAGATGGAGTATTTGAAACGCTGACAAATTTGGAGTTGCTAT CACTATCTTTCAATTCTCTTTCACACGTGCCACCCAAACTGCCAAGCTCCCTACGCAAACTTTTTCTGAGCAACA CCCAGATCAAATACATTAGTGAAGAAGATTTCAAGGGATTGATAAATTTAACATTACTAGATTTAAGCGGGAACT GTCCGAGGTGCTTCAATGCCCCATTTCCATGCGTGCCTTGTGATGGTGCTTCAATTAATATATAGATCGTTTTG CTTTTCAAAACTTGACCCAACTTCGATACCTAAACCTCTCTAGCACTTCCCTCAGGAAGATTAATGCTGCCTGGT TTAAAAATATGCCTCATCTGAAGGTGCTGGATCTTGAATTCAACTATTTAGTGGGAGAAATAGTCTCTGGGGCAT TTTTAACGATGCTGCCCCGCTTAGAAATACTTGACTTGTCTTTTAACTATAAAGGGGAGTTATCCACAGCATA TTAATATTTCCAGAAACTTCTCTAAACTTTTGTCTCTACGGGCATTGCATTTAAGAGGTTATGTGTTCCAGGAAC TCAGAGAAGATGATTTCCAGCCCCTGATGCAGCTTCCAAACTTATCGACTATCAACTTGGGTATTAATTTTATTA AGCAAATCGATTTCAAACTTTTCCAAAATTTCTCCAATCTGGAAATTATTTACTTGTCAGAAAACAGAATATCAC CGTTGGTAAAAGATACCCGGCAGAGTTATGCAAATAGTTCCTCTTTTCAACGTCATATCCGGAAACGACGCTCAA CAGATTTTGACTCCACATTCGAACTTTTATCATTTCACCCGTCCTTTAATAAAGCCACAATGTGCTGCTT ATGGAAAAGCCTTAGATTTAAGCCTCAACAGTATTTTCTTCATTGGGCCAAACCAATTTGAAAATCTTCCTGACA TTGCCTGTTTAAATCTGTCTGCAAATAGCAATGCTCAAGTGTTAAGTGGAACTGAATTTTCAGCCATTCCTCATG TCAAATATTTGGATTTGACAAACAATAGACTAGACTTTGATAATGCTAGTGCTCTTACTGAATTGTCCGACTTGG AAGTTCTAGATCTCAGCTATAATTCACACTATTTCAGAATAGCAGGCGTAACACATCATCTAGAATTTATTCAAA ATTTCACAAATCTAAAAGTTTTAAACTTGAGCCACAACAACATTTATACTTTAACAGATAAGTATAACCTGGAAA GCAAGTCCCTGGTAGAATTAGTTTTCAGTGGCAATCGCCTTGACATTTTGTGGAATGATGATGACAACAGGTATA TCTCCATTTTCAAAGGTCTCAAGAATCTGACACGTCTGGATTTATCCCTTAATAGGCTGAAGCACATCCCAAATG AAGCATTCCTTAATTTGCCAGCGAGTCTCACTGAACTACATATAAATGATAATATGTTAAAGTTTTTTAACTGGA CATTACTCCAGCAGTTTCCTCGTCTCGAGTTGCTTGACTTACGTGGAAACAACTACTCTTTTTAACTGATAGCC TATCTGACTTTACATCTTCCCTTCGGACACTGCTGCTGAGTCATAACAGGATTTCCCACCTACCCTCTGGCTTTC TTTCTGAAGTCAGTAGTCTGAAGCACCTCGATTTAAGTTCCAATCTGCTAAAAAACAATCAACAAATCCGCACTTG AAACTAAGACCACCACCAAATTATCTATGTTGGAACTACACGGAAACCCCTTTGAATGCACCTGTGACATTGGAG ATTTCCGAAGATGGATGGATGAACATCTGAATGTCAAAATTCCCAGACTGGTAGATGTCATTTGTGCCAGTCCTG GGGATCAAAGAGGGAAGAGTATTGTGAGTCTGGAGCTAACAACTTGTGTTTCAGATGTCACTGCAGTGATATTAT TTTTCTTCACGTTCTTTATCACCACCATGGTTATGTTGGCTGCCCTGGCTCACCATTTGTTTTACTGGGATGTTT GGTTTATATATATGTGTGTTTTAGCTAAGGTAAAAGGCTACAGGTCTCTTTCCACATCCCAAACTTTCTATGATG AGAGCCGAGACAAAAACGTTCTCCTTTGTCTAGAGGAGAGGGATTGGGACCCGGGATTGGCCATCATCGACAACC TCATGCAGAGCATCAACCAAAGCAAGAAAACAGTATTTGTTTTAACCAAAAAATATGCAAAAAGCTGGAACTTTA AAACAGCTTTTTACTTGGCTTTGCAGAGGCTAATGGATGAGAACATGGATGTGATTATATTTTATCCTGCTGGAGC CAGTGTTACAGCATTCTCAGTATTTGAGGCTACGGCAGCGGATCTGTAAGAGCTCCATCCTCCAGTGGCCTGACA ACCCGAAGGCAGAAGGCTTGTTTTGGCAAACTCTGAGAAATGTGGTCTTGACTGAAAATGATTCACGGTATAACA ${\tt ATATGTATGTCGATTCCATTAAGCAATAC} \underline{{\tt TAA}} {\tt CTGACGTTAAGTCATGATTTCGCGCCATAATAAAGATGCAAAG}$ GAATGACATTTCTGTATTAGTTATCTATTGCTATGTAACAAATTATCCCAAAACTTAGTGGTTTAAAACAACACA TTTGCTGGCCCACAGTTTTTGAGGGTCAGGAGTCCAGGCCCAGCATAACTGGGTCCTCTGCTCAGGGTGTCTCAG AGGCTGCAATGTAGGTGTTCACCAGAGACATAGGCATCACTGGGGTCACACTCATGTGGTTGTTTTCTGGATTCA ATCAGAGCTAGCAAAAAAGAGAGGTTGCTAGCAAGATGAAGTCACAATCTTTTGTAATCGAATCAAAAAAGTGAT ATCTCATCACTTTGGCCATATTCTATTTGTTAGAAGTAAACCACAGGTCCCACCAGCTCCATGGGAGTGACCACC TCAGTCCAGGGAAAACAGCTGAAGACCAAGATGGTGAGCTCTGATTGCTTCAGTTGGTCATCAACTATTTTCCCT TGACTGCTGTCCTGGGATGGCCTGCTATCTTGATGATAGATTGTGAATATCAGGAGGCAGGGATCACTGTGGACC ATCTTAGCAGTTGACCTAACACATCTTCTTTTCAATATCTAAGAACTTTTGCCACTGTGACTAATGGTCCTAATA TTAAGCTGTTGTTTATATTTATCATATATCTATGGCTACATGGTTATATTATGCTGTGGTTGCGTTCGGTTTTAT TTACAGTTGCTTTTACAAATATTTGCTGTAACATTTGACTTCTAAGGTTTAGATGCCATTTAAGAACTGAGATGG ATAGCTTTTAAAGCATCTTTTACTTCTTACCATTTTTTAAAAGTATGCAGCTAAATTCGAAGCTTTTGGTCTATA

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSYPCDEKKQNDSVIAECSNRRLQEVPQTVG KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHQNGNPGIQSNGLNITDGAFLNL KNLRELLLEDNOLPOIPSGLPESLTELSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEEDFKGLINL TLLDLSGNCPRCFNAPFPCVPCDGGASINIDRFAFONLTOLRYLNLSSTSLRKINAAWFKNM PHLKVLDLEFNYLVGEIVSGAFLTMLPRLEILDLSFNYIKGSYPOHINISRNFSKLLSLRAL HLRGYVFQELREDDFQPLMQLPNLSTINLGINFIKQIDFKLFQNFSNLEIIYLSENRISPLV KDTROSYANSSSFORHIRKRRSTDFEFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI GPNOFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDLEV LDLSYNSHYFRIAGVTHHLEFIONFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL DILWNDDDNRYISIFKGLKNLTRLDLSLNRLKHIPNEAFLNLPASLTELHINDNMLKFFNWT LLOOFPRLELLDLRGNKLLFLTDSLSDFTSSLRTLLLSHNRISHLPSGFLSEVSSLKHLDLS SNLLKTINKSALETKTTTKLSMLELHGNPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP GDORGKSIVSLELTTCVSDVTAVILFFFTFFITTMVMLAALAHHLFYWDVWFIYNVCLAKVK GYRSLSTSQTFYDAYISYDTKDASVTDWVINELRYHLEESRDKNVLLCLEERDWDPGLAIID NLMOSINOSKKTVFVLTKKYAKSWNFKTAFYLALQRLMDENMDVIIFILLEPVLQHSQYLRL RQRICKSSILQWPDNPKAEGLFWQTLRNVVLTENDSRYNNMYVDSIKQY

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 826-848

 ${\tt CCAGGTCCAACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT}$ CGACCTCGACCCACGCGTCCGCCAAGCTGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA ${\tt CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC}$ AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCGGCCACCATGGCCACGCCTGGGC TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA GCAGCTCCTGCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA $\tt GGCCACCCGCCTGGAGGCACAGGCC{\bf ATG} GGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT$ CTGGTGTTGGCAGTGGGCGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGCTGT CCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCGTGCAGCGTGTGTACCAGCCCTTCCTCA CCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC CGCAGCCTGGGCTGGCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGAC CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGA GCTGTGTCCAGCCTGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA GATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGCCGG CAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC CCAAGGGGGGCCCCCAGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAA GAAGTGCAGAGGCTGCAGGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGC CCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC GAGGAGCAGCTGGGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTG GACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATGCCCCAACATGCTGGGGGTCCAG AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGCCTTCCTCCTCCTCCTCCCCC ${\tt TTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC}$ CCCTGGCTACCCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAG GCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAACGTGA CGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAAT

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR CPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKGGPPRVA PNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC AGCAGCATCAGAGCAGCCCCTGTGGTTGGCAGCAAAGTTCAGCTTGGCTGGGCCCGCTGTGA GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC AGTGGATGAGCAACCCAACGGGGGCCCGGGGAGGGAACTGGCCCCGAGGGAGAGCAACCCC AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG $\tt CACAGGTGGCCCCACCACCCGGAGGAGCAGCTCCTGCCCCTGTCCGGGGGATGACTGATTC$ TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGCC TCTCAGGAGGTGCTGATGTGGCTTCTGGTGTTGGCAGTGGGCGCACAGAGCACGCCTA CCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCG TGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTAC CGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCTGCCAGGCCTCGCTA CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGGCCTGTGGAGCAGCAATAT GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCCTGCA GGATGGCGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTG TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCC TGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT GGAGGAGAGCTGCAGCTGGTGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGAC CTCGTGACTGCCCAGCGCTCCAGGCTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATG CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC AGGGCCTTCCTCCTCCTCCTCCCCTTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCACCCTGGCTACCCCAACGGCA TCCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC ${\tt CCATGGCACAGGCCAGGCCGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGAC}$ CCCCAGCACAATAAAAATGAAACGTG

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCGGAGGAGCAGCTCCTGC CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC $\tt CTGGAGGCACAGGCC{\color{red} \underline{\textbf{A}}\textbf{T}\underline{\textbf{G}}} AGGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTTTGGC$ AGTGGGCGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACG GGGACCCTGTCTCCGAGTCGTTCGTGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGAC GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG GCTGGCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC CCTGGCCGCTGCCGCTGCCCGGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA ATGCAGTGCTAGGAGGGGGGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACA GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCC $\tt GGGGTCCTGCTGCAAGAAAGACTCG\underline{TGA}CTGCCCAGCGCCCCAGGCTGGACTGAGCCCC$ TCACGCCGCCCTGCAGCCCCCATGCCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG GGGTGACTGAGCGGAAGGCCAGGCAGGCCTTCCTCCTCTCCTCCTCCCCTTCCTCGGGAG GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC CCCACCTGGCTACCCCAACGCCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAACGTG

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTCQSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

GGTTGCCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCTTGTCAGGAGGAGACAGCCTCCCGGCCCGGGGAG AGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTCCTGGTCTCCCCTTCTCCCGCTGGGCCGGTTTATCGGGAGG AGATTGTCTTCCAGGGCTAGCAATTGGACTTTTGATGATGTTTTGACCCAGCGCAGGAATAGCAGGCAACGTGAT ${\tt TTCAAAGCTGGGCTCAGCCTCTGTTTCTTCTCTGTGTAATCGCAAAACCCATTTTGGAGCAGGAATTCCAATC} \underline{{\tt A}}$ ATGGCCGCGTCATGATGGCCCGGCAAAAGGGCATTTTCTACCTGACCCTTTTCCTCATCCTGGGGACATGTACAC TCCTTTTCTCCATGGCTACACTGTTGAGGACCAGCTTCAGTGACCCTGGAGTGATTCCTCGGGCGCTACCAGATG AAGCAGCTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGCGACCACCGCCTCGTA TCAAGAATTTCCAGATAAACAACCAGATTGTGAAACTGAAATACTGTTACACATGCAAGATCTTCCGGCCTCCCC CTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAATCGCGTCCAGAATCCCTACAGCC ${\tt ATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGTGGCCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGTA}$ TTTTGCCACTGGAGGAAAGTGGAAGTCGACCTCCCAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCC CAGCCCCCACAGAACACCTGAACTCAAATGAGATGCCGGAGGACAGCACTCCCGAAGAGATGCCACCTCCAG TAATTAGGGCTATGAGAGATTTCAGGTGAGAAGTTAAACCTGAGACAGGAGCAAGTAAGCTGTCCCTTTTAACT GTTTTTCTTTGGTCTTTAGTCACCCAGTTGCACACTGGCATTTTCTTGCTGCAAGCTTTTTTAAATTTCTGAACT CAAGGCAGTGGCAGAAGATGTCAGTCACCTCTGATAACTGGAAAAATGGGTCTCTTGGGCCCTGGCACTGGTTCT CCATGGCCTCAGCCACAGGGTCCCCTTGGACCCCCTCTCTTCCCTCCAGATCCCAGCCCTCCTGCTTGGGGTCAC TGGTCTCATTCTGGGGCTAAAAGTTTTTGAGACTGGCTCAAATCCTCCCAAGCTGCTGCACGTGCTGAGTCCAGA GGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTTCTTGGGGTCTTCAGGACTGAAGAGAGGAGGAAG TGGGGTCAGAAGATTCTCCTGGCCACCAAGTGCCAGCATTGCCCACAAATCCTTTTAGGAATGGGACAGGTACCT CAGGAATGCCAGTAATAAAAGTCTGCACTTTGGTCATTTCTTTTCCTCAGAGGAAGCCCGAGTGCTCACTTAAAC ACTATCCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG $\tt CGGCTGAGTGAGGGAAAGCCCAGCACTGCTGCCCTCTCGGGTAACTCACCCTAAGGCCTCGGCCCACCTCTGGCT$ ATGGTAACCACACTGGGGGCTTCCTCCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCCAGAGCCACTT $\tt CACCTGGGGGTGGGCTGTGGCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTCAGGGAAGAAGATTTATGT$ ATTATATGTGGCTATATTTCCTAGAGCACCTGTGTTTTCCTCTTTCTAAGCCAGGGTCCTGTCTGGATGACTTAT GCGGTGGGGGAGTGTAAACCGGAACTTTTCATCTATTTGAAGGCGATTAAACTGTGTCTAATGCA

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTLFLILGTCTLFFAFECRYLAV QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHCPWVGNCVGKRNYRYFYL FILSLSLLTIYVFAFNIVYVALKSLKIGFLETLKETPGTVLEVLICFFTLWSVVGLTGFHTF LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSR PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPPEPPQEAAEAEK

Putative transmembrane domains:

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

AAAACCCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT
CCCACAGAGCNCTTCGACCATCACTGCCCCTGGGTGGGGAATTGTGTTTGGAAAGAGGAACTA
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCCNCCTCACAATCTATGTCTTCGCCTTCA
ACATCGT

GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA TCTATCAGGAAAGAAAGAAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAGAAGAAGA AAAAAAATC**ATG**AAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC GGGGCTGCTCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCG CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTC TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACA TTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA GAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTG AACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC ATCATGCTATTTGGTCCAGGCGCGCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGG CTGCGTCTGGCTGCTCTTCTGGTCTTGCACCTGCTTCTCAAATTT**TGA**TGTGAGTGCC CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA AATTTGAGGGAGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAAGAAATTGAA AATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA GGGCTCAGCCTCTCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA AAAAA

MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL
ÈIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAV
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF

Signal peptide:

amino acids 1-28

GAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACACA
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATT
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG
ACCAGAG

ATGGCTGGTGACGGCGGGCCGGGCAGGGGACCGGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA GCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCCACAGCACCTGCCTTACA GAGGCCTGCATTCGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCCTGTGAGGACTTTTAC CAGTTCTCCTGTGGGGGCTGGATTCGGAGGAACCCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAG CAGAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCCAGCCACTGAGA GACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACTTTATGGAGGTGTTGAAG GCAGTAGCAGGGACCTACAGGGCCACCCCATTCTTCACCGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGC AATGTTATCCAGGTGGACCAGTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAACATCACAGTGCCCCAGGACCAGCGGCGCGAC GAGGAGAAGATCTACCACAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTC CAGGTGTCAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCTCTATGGCACTAAGAAG TCCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTTGGGGTCACTCTTC GTGAAGGCCACGTTTGACCGGCAAAGCAAAGAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTTGAG GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCAGATGCCATCTAT GATATGATTGGTTTCCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT GAAGATTCTTTCTTCCAAAACATGTTGAATTTGTACAACTTCTCTGCCAAGGTTATGGCTGACCAGCTCCGCAAG $\tt CCTCCCAGCCGAGACCAGTGGAGCATGACCCCCCAGACAGTGAATGCCTACTACCTTCCAACTAAGAATGAGATC$ GTCTTCCCCGCTGGCATCCTGCAGGCCCCCTTCTATGCCCGCAACCACCCCAAGGCCCTGAACTTCGGTGGCATC GGTGTGGTCATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTG CGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAGTACAATCAA TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACATTACTGACAACGGGGGGCTGAAG GCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC AACCACCAGCTCTTCTTCGTGGGATTTGCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGG CTGGTGACCGACCCCCACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACTCCCGTGACTTCCTGCGG CACTTCGGCTGCCCTGTCGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACCTGGATCAGGGGA GAAATGGCCAGCTGTCACCAGACCTGGGGCAGCTCTCCTGACAAAGCTGTTTGCTCTTGGGTTGGGAGGAAGCAA ${\tt ATGCAAGCTGGGTCTAGTCCCTCCCCCCCACAGGTGACATGAGTACAGACCCTCCTCAATCACCACATTG}$ $\tt TGCCTCTGCTTTGGGGGTGCCCTGCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGTGTCACCCT$

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSH
STCLTEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQA
ILKHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDN
FMEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSRDYYLNRTANEKVLTAY
LDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP
SMDWLEFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL
DRRFESAQEKLLETLYGTKKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI
SEIRTAFEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF
FQNMLNLYNFSAKVMADQLRKPPSRDQWSMTPQTVNAYYLPTKNEIVFPAGILQAPFYARNH
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQV
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCS
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNPGQLCEVW

Type II Transmembrane domain:

amino acids 32-57

CGGCTCCGGCCGGCCGGCGCGCCCAGAGCCCCCGTGCTGCCCATCCGTTCTGAGAAGGAGCCGCTGCC CGTTCGGGGAGCGGCAGGTAGGTGGGCGCCCGGGGGAGGCGCGGGGGAGTCGGGCTCGGGCGAGTCAGCGC GCGGTGCCTGGGACCCGGGGCAGCCCCCGGGGCGCACACGGCGCGAGCTGGGCAGCGCCCCAGC CAAGCCCGTCCCCGCAGGCTGCACCTTCGGCGGGAAGGTCTATGCCTTGGACGAGACGTGGCACCCGGACCTAGG GGAGCCATTCGGGGTGATGCGCTGCGTGCTGCGCCTGCGAGGCGCAGTGGGGTCGCCGTACCAGGGGCCCTGG CAGGGTCAGCTGCAAGAACATCAAACCAGAGTGCCCAACCCCGGCCTGTGGGCAGCCGCGCCAGCTGCCGGGACA CTGCTGCCAGACCTGCCCCAGGACTTCGTGGCGCTGCTGACAGGGCCGAGGTCGCAGGCGGTGGCACGAGCCCG AGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCCTACAGGCGGCTGGACCGCCCTACCAGGATCCGCTT TCTAGAAGGCCCCCACCAGCAGGGCGTAGGGGGCATCACCCTGCTCACTCTCAGTGACACAGAGGACTCCTTGCA TTTTTTGCTGCTCTTCCGAGGCCTTGCAGGACTAACCCAGGTTCCCTTGAGGCTCCAGATTCTACACCAGGGGCA GCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCCAGGAACCAGGCTTTGCTGAGGTGCTGCCCAACCTGACAGT CAGTGGACACATTGCTGCCAGGAAGAGCTGCGACGTCCTGCAAAGTGTCCTTTGTGGGGCTAATGCCCTGATCCC AGTCCAAACGGGTGCTGCCGGCTCAGCCAGCCTCACTCTGCTAGGAAATGGCNCCCTGATCCTCCAGGTGCAATT GGTAGGGACAACCAGTGAGGTGGTGGCCATGACACTGGAAACCAAGCCTCAGCGGAGGGATCAGCCCACTGTCCT GTGCCACATGGCTGGCCTATCCTCCCTGCCCCCAGGCCGTGGGTATCTGCCCTGGGCTGGGTGCCCGAGGGGC TCATATGCTGCTGCAGAATGAGCTCTTCCTGAACGTGGGCACCAAGGACTTCCCAGACGAGAGGACTTCGGGGGCA $\tt CCCTGTGAAGAGCCAAGCAGGGCACGCCTGGCTTTCCTTGGATACCCACTGTCACCTGCACTATGAAGTGCT$ GCTGGCTGGGCTTGGTGGCTCAGAACAAGGCACTGTCACTGCCCACCTCCTTGGGCCTCCTGGAACGCCAGGGCC TCGGCGGCTGCTGAAGGGATTCTATGGCTCAGAGGCCCAGGGTGTGGTGAAGGACCTGGAGCCGGAACTGCTGCG GCACCTGGCAAAAGGCATGGCTTCCCTGATGATCACCACCAAGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGCCT GCGGGCGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCCGCCTGTGGTGCCTGGTCTCCCGGCCCTAGCGCCCGC CAAACCTGGTGGTCCTGGGCGGCCCCGAGACCCCAACACTGCTTCTTCGAGGGGCAGCAGCGCCCCCACGGGGC TCGCTGGGCGCCCAACTACGACCCGCTCTGCTCACTCTGCACCTGCCAGAGACGAACGGTGATCTGTGACCCGGT GGTGTGCCCACCGCCAGCTGCCCACACCCGGTGCAGGCTCCCGACCAGTGCTGCCCTGTTTGCCCTGGCTGCTA GTGTGCTGTCTGCACCTGCAAGCAGGGGGGCACTGGAGAGGTGCACTGTGAGAAGGTGCAGTGTCCCCGGCTGGC CTGTGCCCAGCCTGTGCGTGTCAACCCCACCGACTGCTGCAAACAGTGTCCAGGTGAGGCCCACCCCCAGCTGGG GGACCCCATGCAGGCTGATGGGCCCCGGGGCTGCCGTTTTGCTGGGCAGTGGTTCCCAGAGAGTCAGAGCTGGCA CCCCTCAGTGCCCCCGTTTGGAGAGATGAGCTGTATCACCTGCAGATGTGGGGTAAGTGGGGAGCAGAGGCTTGT GTGAGGTGGGTACTGGGAGCCTGGTCTGGAGTAGGGAGACCTTCCCAGGGAGGTCCCTGAAGAAGCTGAAGGTCA GGGATGACTGTTCACTGCCACTGTCCTGTGGCTCGGGGAAGGAGAGTCGATGCTGTTCCCGCTGCACGGCCCACC GGAAGGGAGCACTCACTGTGTGCAGGAACAGTGCAGCCTCACAAGTGCCATTCCAATCCACCCTCACAGCA ACCTGGTGGAATTGTTATTTATGACCTTTTCTTTACAAATGAGATTTCTGAAGCTCAGAGAAATTAAGCAACGAG ATGAAGGTCACCCAGCTGTGTGCACTGACCTGTTTAGAAAATACTGGCCTTTCTGGGACCAAGGCAGGGATGCTT $\tt CCCAGTGCCTTTGCTCCTGTCCTGCCTCTACTCCCACCCCCACTACCTCTGGGAACCACAGCTCCACAAGGGG$ GAGAGGCAGCTGGGCCAGACCGAGGTCACAGCCACTCCAAGTCCTGCCACCCTCGGCCTCTGTCCTGGAA GCCCCACCCCTTTCTTCCTGTACATAATGTCACTGGCTTGTTGGGATTTTTAATTTATCTTCACTCAGCACCAAG GGCCCGGACACTCCACTCCTGCTGCCCCTGAGCTGAGCAGAGTCATTATTGGAGAGTTTTTTTATTAAAAC $\tt CGTGGCNNTTGGCTGGCATNCCTGGGTTCCGCAGAGGGGGCTGGGGATGGTTCTTGAGATGGTCTAGAGACTCAAG$ AATTTAGGGAAGTAGAAGCAGGATTTTGACTCAAGTTTAGTTTCCCACATCGCTGGCCTGTTTGCTGACTTCATG TTTGAAGTTGCTCCAGAGAGAGAATCAAAGGTGTCACCAGCCCCTCTCTCCCTTCCCTTCCCTTCCCTTTCT TTCCCTCCCCTCCCCTCCCCTCC

GGCCGAGCGGGGGTGCTGCGCGGCGGCCGTGATGGCTGACGGCGGGGCCGGGCAGGGGA CCGGGGCCGGGCCCGGGGGCCGGGCCGGGGCCCTGAATCACCGCCTGGCCCGACTCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAACGTGGGATTCCAGAAGGG GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA TCCCACAGCACCTGCCTTACAGAGGCCTGCATTCGAGTGGCTGGAAAAATCCTGGAGTCCCT GGACCGAGGGGTGAGCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTCGGA GGAACCCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTCTTCAC CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC ATCTTCCGAACCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTCACCTAGTGAACAAACTGCCCCT TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTCG GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTCGATGGGTTCATGGACCT AGATAGGCTGATAACAAAGCTCACAAGAGGGTCCTGAGGATTCAGGAGAGACTTATGGAGCC AGCAAAGTCTTCCTGAAGAGATTGCATTTGAGCCAGGTCCTGTAG

ATGCCTACTACCTTCCAACTAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC TTCTATGCCCGCAACCACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGAACCTGCGGC CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAG TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG GGGAGGAGCAGCTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT CCACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACTCCCGTGACTTCCTGCGGC ACTTCGGCTGCCCTGTCGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC TGGATCAGGGGAGAAATGGCCAGCTGTCACCAGACCTGGGGCAGCTCTCCTGACAAAGCTGT GGTGACATGAGTACAGACCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCCT GTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCCTCTTCTGTCCCCAGGCTCACT CAGCCTGCGGCCATGGGGCCTGCCGTGCCCCACTGTGACCCACAGGCCTGGGTGGTG ${ t TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCGCACTTAGGGGTGGACTCAGCTCTGTC}$ TGGCTCACCCTCACGGGCTACCCCCACCTCACCCTGTGCTCCTTGTGCCACTGCTCCCAGTG CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCATATGTGTAGCGGGTACTGGTTCCTGT GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA GAGCAGGGAAAAGGAACAGAGTTTATTTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT TGGCCCTTATAGGACC

CCCACGCGTCCGAGCCGCCGAGAATTAGACACACTCCGGACGCGGCCAAAAGCAACCGAGA AAAAAAAAAAATCCTGTGGCGCGCCGCCTGGTTCCCGGGAAGACTCGCCAGCACCAGGGGG TGGGGGAGTGCGAGCTGAAAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGGATGGAC<u>ATG</u>ATG CTGTTGGTGCAGGGTGCTTGTTGCTCGAACCAGTGGCTGCCGGCGGTGCTCCTCAGCCTGTG CTGCCTGCTACCCTCCTGCCTCCGGCTGGACAGAGTGTGGACTTCCCCTGGGCGGCCGTGG ACAACATGATGGTCAGAAAAGGGGACACGGCGGTGCTTAGGTGTTATTTGGAAGATGGAGCT TCAAAGGGTGCCTGGCTGAACCGGTCAAGTATTATTTTTGCGGGAGGTGATAAGTGGTCAGT GGATCCTCGAGTTTCAATTTCAACATTGAATAAAAGGGACTACAGCCTCCAGATACAGAATG ATGCAGGTGCATCTAACTGTGCAAGTTCCTCCTAAGATATATGACATCTCAAATGATATGAC CGTCAATGAAGGAACCAACGTCACTCTTACTTGTTTGGCCACTGGGAAACCAGAGCCTTCCA TTTCTTGGCGACACATCTCCCCATCAGCAAAACCATTTGAAAATGGACAATATTTGGACATT TATGGAATTACAAGGGACCAGGCTGGGGAATATGAATGCAGTGCGGAAAATGCTGTGTCATT CCCAGATGTGAGGAAAGTAAAAGTTGTTGTCAACTTTGCTCCTACTATTCAGGAAATTAAAT CTGGCACCGTGACCCCGGACGCAGTGGCCTGATAAGATGTGAAGGTGCAGGTGTGCCGCCT CCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCTCTTCAATGGCCAACAAGGAATTATTAT TCAAAATTTTAGCACAAGATCCATTCTCACTGTTACCAACGTGACACAGGAGCACTTCGGCA CCAAGTACAGCCCAGTATGGAATTACCGGGAGCGCTGATGTTCTTTTCTCCTGCTGGTACCT TGTGTTGACACTGTCCTCTTTCACCAGCATATTCTACCTGAAGAATGCCATTCTACAA<u>TAA</u>A TTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCTGAAAGTGCTGATGGCTGGATCCAATCT GGTACAGTTTGTTAAAAGCAGCGTGGGATATAATCAGCAGTGCTTACATGGGGATGATCGCC TTCTGTAGAATTGCTCATTATGTAAATACTTTAATTCTACTCTTTTTTGATTAGCTACATTA CCTTGTGAAGCAGTACACATTGTCCTTTTTTTAAGACGTGAAAGCTCTGAAATTACTTTTAG AGGATATTAATTGTGATTTCATGTTTGTAATCTACAACTTTTCAAAAGCATTCAGTCATGGT CTGCTAGGTTGCAGGCTGTAGTTTACAAAAACGAATATTGCAGTGAATATGTGATTCTTTAA GGCTGCAATACAAGCATTCAGTTCCCTGTTTCAATAAGAGTCAATCCACATTTACAAAGATG CATTTTTTTTTTTTTTTTTTTAAAAAAGCAAATAATATTTCCTTCAGATTATTTCTTCAAAATA TAACACATATCTAGATTTTTCTGCTTGCATGATATTCAGGTTTCAGGAATGAGCCTTGTAAT ATAACTGGCTGTGCAGCTCTGCTTCTCTTTCCTGTAAGTTCAGCATGGGTGTGCCTTCATAC AATAATATTTTCTCTTTGTCTCCAACTAATATAAAATGTTTTGCTAAATCTTACAATTTGA AAGTAAAAATAAACCAGAGTGATCAAGTTAAACCATACACTATCTCTAAGTAACGAAGGAGC TATTGGACTGTAAAAATCTCTTCCTGCACTGACAATGGGGTTTGAGAATTTTGCCCCACACT AACTCAGTTCTTGTGATGAGAGACAATTTAATAACAGTATAGTAAATATACCATATGATTTC TTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGAAATCATTCCCTTTAAAATGACAGCACA GTCCACTCAAAGGATTGCCTAGCAATACAGCATCTTTTCCTTTCACTAGTCCAAGCCAAAAA TTTTAAGATGATTTGTCAGAAAGGGCACAAAGTCCTATCACCTAATATTACAAGAGTTGGTA AGCGCTCATCATTAATTTTATTTTGTGGCAGGTATTATGACAGTCGACCTGGAGGGTATGGA TATGGATATGGACGTTCCAGAGACTATAATGGCAGAAACCAGGGTGGTTATGACCGCTACTC AGGAGGAAATTACAGAGACAATTATGACAACTGAAATGAGACATGCACATAATATAGATACA CAAGGAATAATTTCTGATCCAGGATCGTCCTTCCAAATGGCTGTATTTATAAAGGTTTTTGG AGCTGCACTGAAGCATCTTATTTTATAGTATATCAACCTTTTGTTTTTAAATTGACCTGCCA

MMLLVQGACCSNQWLAAVLLSLCCLLPSCLPAGQSVDFPWAAVDNMMVRKGDTAVLRCYLED
GASKGAWLNRSSIIFAGGDKWSVDPRVSISTLNKRDYSLQIQNVDVTDDGPYTCSVQTQHTP
RTMQVHLTVQVPPKIYDISNDMTVNEGTNVTLTCLATGKPEPSISWRHISPSAKPFENGQYL
DIYGITRDQAGEYECSAENAVSFPDVRKVKVVVNFAPTIQEIKSGTVTPGRSGLIRCEGAGV
PPPAFEWYKGEKKLFNGQQGIIIQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTTNASLPL
NPPSTAQYGITGSADVLFSCWYLVLTLSSFTSIFYLKNAILQ

Important features of the protein:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 326-345

N-glycosylation sites.

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

Casein kinase II phosphorylation site.

amino acids 147-151, 208-212, 224-228

Tyrosine kinase phosphorylation site.

amino acids 178-186

N-myristoylation sites.

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297, 302-308, 319-325

Myelin P0 protein:

amino acids 92-121

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTTCTGCTGG CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGA CGAGCTCTTGAGTGAGACCCAACAAGCTGCTTTTCACCAAATTGCAATGGAGCCTTTCGAAA TCAATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACTTCTCCCTAGCTGTGGTGGTCATC TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC GCGGCTCCGGGTCCTGGAGATGTATTTCCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT CCTTCTCCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTG CAAGTCCTGCAGGCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGT AGACAACTTCACTCAGAACCCAGGGATGTTCAGAATCAAAGGTGAACAAGGCGCCCCAGGTC TTCAAGGTCACAAGGGGGCCATGGGCATGCCTGGTGCCCTGGCCCGCCGGGACCACCTGCT GAGAAGGGAGCCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCCTCGGGACCCCAAGG CCCACCGGGAGTCAAGGGAGAGGCGGGCCTCCAAGGACCCCAGGGTGCTCCAGGGAAGCAAG GAGCCACTGGCACCCCAGGACCCCAAGGAGAGAGGGCAGCAAAGGCGATGGGGGTCTCATT GGCCCAAAAGGGGAAACTGGAACTAAGGGAGAGAAAGGAGACCTGGGTCTCCCAGGAAGCAA AGGGGACAGGGCATGAAAGGAGATGCAGGGGTCATGGGGCCTCCTGGAGCCCAGGGGAGTA AAGGTGACTTCGGGAGGCCAGGCCCACCAGGTTTGGCTGGTTTTCCTGGAGCTAAAGGAGAT CAAGGACAACCTGGACTGCAGGGTGTTCCGGGCCCTCCTGGTGCAGTGGGACACCCAGGTGC CAAGGGTGAGCCTGGCAGTGCTGGCTCCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGA GTCCAGGAGCCACAGGCCTGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGA AGAAAAGGAGAATCAGGAGTTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCAGG GCTGGCAGGTCCCAAGGGAGCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAAGGTGAAAGGGTGAAAACTCAGTGTCC GTCAGGATTGTCGGCAGTAGTAACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGG GACAATTTGCGATGACGAGTGGCAAAATTCTGATGCCATTGTCTTCTGCCGCATGCTGGGTT GTTCAGTGTCGGGGCACGGAGAGTACCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCA TGACTGCAGCCACGAGGAGGACGCAGGCGTGGAGTGCAGCGTCTGACCCGGAAACCCTTTCA CTTCTCTGCTCCGAGGTGTCCTCGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT TCCCTGGGGACAACTGAGCAGCCTCTGGAGAGGGGCCATTAATAAAGCTCAACATCATTGA

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

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Transmembrane domain:

amino acids 47-66 (type II)

N-glycosylation sites.

amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.

amino acids 432-440

N-myristoylation sites.

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352, 400-406, 441-447, 475-481, 490-496, 515-521

Amidation site.

amino acids 360-364

Leucine zipper pattern.

amino acids 56-78

Speract receptor repeat

amino acids 422-471, 488-519

Clq domain proteins.

amino acids 151-184, 301-334, 316-349

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758</pre>

<subunit 1 of 1, 98 aa, 1 stop

<MW: 11081, pI: 6.68, NX(S/T): 1

MKLMVLVFTIGLTLLLGVQAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHFWDG KGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-76

Tyrosine kinase phosphorylation site.

amino acids 63-71

CCCACGCGTCCGCGGACGCGTGGGCTCGGACCCCAGGTCTGGAGCGAATTCCAGCCTGCAGGG CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCCGCCGTGGTGGTTGGAGGGC TAAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTTTTGGAT GAATTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGC AGGAACAGAACAAACTTTCAGCTTGCAAAGCAAATTCAATCCCAGTGGAAAGAATTTGGCC TGGATTCTGTTGAGCTAGCTCATTATGATGTCCTGTTGTCCTACCCAAATAAGACTCATCCC AACTACATCTCAATAATTAATGAAGATGGAAATGAGATTTTCAACACATCATTATTTGAACC ACCTCCTCCAGGATATGAAAATGTTTCGGATATTGTACCACCTTTCAGTGCTTTCTCTCCTC AAGGAATGCCAGAGGGCGATCTAGTGTATGTTAACTATGCACGAACTGAAGACTTCTTTAAA TTGGAACGGGACATGAAAATCAATTGCTCTGGGAAAATTGTAATTGCCAGATATGGGAAAGT TTTCAGAGGAAATAAGGTTAAAAATGCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACT CCGACCCTGCTGACTACTTTGCTCCTGGGGTGAAGTCCTATCCAGACGGTTGGAATCTTCCT GGAGGTGGTGTCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACC AGGTTACCCAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGAGGCTGTTGGTCTTCCAA GTATTCCTGTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGC TCAGCACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG CTTTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA $\tt CTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAGCTGT$ CAATTTTGTTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTGAGTGGGCA $_{ij}$ <code>GAGGAGAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTAT</code> $\widetilde{\mathbb{F}}$ AGAAGGAAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTGGTACACAACC ##TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATGAAAGTTGG #ACTAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCCAGGATAAGCAAATTGGGATCTGG $rac{1}{2}$ AAATGATTTTGAGGTGTTCTTCCAACGACTTGGAATTGCTTCAGGCAGAGCACGGTATACTA #AAAATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAACATAT GAGTTGGTGGAAAAGTTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCCAGGTTCG _AGGAGGGATGGTGTTTGAGCTAGCCAATTCCATAGTGCTCCCTTTTGATTGTCGAGATTATG **T**TGTAGTTTTAAGAAAGTATGCTGACAAAATCTACAGTATTTCTATGAAACATCCACAGGAA TGAAGACATACAGTGTATCATTTGATTCACTTTTTTCTGCAGTAAAGAATTTTACAGAAAT #GCTTCCAAGTTCAGTGAGAGACTCCAGGACTTTGACAAAAGCAACCCAATAGTATTAAGAA TGATGAATGATCAACTCATGTTTCTGGAAAGAGCATTTATTGATCCATTAGGGTTACCAGAC AGGCCTTTTTATAGGCATGTCATCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTC ATTCCCAGGAATTTATGATGCTCTGTTTGATATTGAAAGCAAAGTGGACCCTTCCAAGGCCT ${\tt TTGAGTGAAGTAGCC} {\tt TAA} {\tt GAGGATTTTTTAGAGAATCCGTATTGAATTTGTGTGTATGTCA}$ CTCAGAAAGAATCGTAATGGGTATATTGATAAATTTTAAAATTGGTATATTTGAAATAAAGT TGAATATTATATAA

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FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756

><subunit 1 of 1, 750 aa, 1 stop

><MW: 84305, pI: 6.93, NX(S/T): 10

MWNLLHETDSAVATARRPRWLCAGALVLAGGFFLLGFLFGWFIKSSNEATNITPKHNMKAFL

DELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTH

PNYISIINEDGNEIFNTSLFEPPPPGYENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFF

KLERDMKINCSGKIVIARYGKVFRGNKVKNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNL

PGGGVQRGNILNLNGAGDPLTPGYPANEYAYRRGIAEAVGLPSIPVHPIGYYDAQKLLEKMG

GSAPPDSSWRGSLKVPYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDRYV

ILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEW

AEENSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSPDEGFEGKSLYES

WTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYET

YELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYSISMKHPQ

EMKTYSVSFDSLFSAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLP

DRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAE

TLSEVA

Signal sequence:

amino acids 1-40

N-glycosylation sites.

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340, 459-463, 476-480, 638-642

Tyrosine kinase phosphorylation sites.

amino acids 363-372, 605-613, 606-613, 617-626

N-myristoylation sites.

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341, 360-366, 427-433, 529-535, 707-713